

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 04:01:33 ; Search time 3521 Seconds
(without alignments)
6339.318 Million cell updates/sec

Title: US-10-045-116-1
Perfect score: 472
Sequence: 1 AGCCACCCAGTCAGCCT.....ACGTTCTCGAAGCTCAAGCA 472

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
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6: gb_pat.*
7: gb_ph.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472	100.0	472	6	BD195486
2	472	100.0	472	6	BD195520
3	472	100.0	472	6	AR451687
4	472	100.0	472	6	AR451733
5	471	99.8	3500	6	AX705342
6	471	99.8	11288	6	AR134885
7	471	99.8	11288	6	AR182304
8	471	99.8	11288	6	AR370519
9	471	99.8	11288	6	AR479027
10	471	99.8	11288	6	AX269130
11	471	99.8	11288	9	HSRCRANTA
12	471	99.8	15056	6	BD195539
13	471	99.8	15056	6	BD224258
14	471	99.8	15056	6	AR266427
15	471	99.8	15056	6	AR474484
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ALIGNMENTS

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LOCUS
DEFINITION Adenovirus vectors containing heterologous transcription regulatory elements and methods of using same.
ACCESSION BD195486
VERSION BD195486.1 GI:33005256
KEYWORDS JP 2002514074-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 472)
AUTHORS Henderson,D.R., Yu,D.C. and Lamparski,H.G.
TITLE Adenovirus vectors containing heterologous transcription regulatory elements and methods of using same
JOURNAL Patent: JP 2002514074-A 7 14-MAY-2002;
COMMENT CALYDON INC
OS Unidentified
PN JP 2002514074-A/7
PD 14-MAY-2002
PF 03-MAR-1998 JP 1998538674
PR 03-MAR-1997 US 60/039762,03-MAR-1997 US 60/039763 PR
04-AUG-1997 US 60/054523,02-MAR-1998 US 09/033556 FI DANIEL R HENDERSON,DE CHAO YU,HENRY G LAMPARSKI PC
C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12N11/08 CC Strandedness: Single;
CC Topology: Linear;
CC Adenovirus vectors containing heterologous transcription CC regulatory
CC elements and methods of using same
FH Key Location/Qualifiers
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FT /organism='Unidentified'.
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Best Local Similarity 100.0%; Pred. No. 5.8e-143;

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LOCUS BD195520 472 bp DNA linear PAT 17-JUL-2003
DEFINITION Adenovirus vectors specific for cells expressing carcinoembryonic
antigens and methods of use thereof.
ACCESSION BD195520
VERSION BD195520.1 GI:33005290
KEYWORDS JP 2002514075-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 472)
AUTHORS Lamparski,H.G., Henderson,D.R. and Schuur,E.R.
TITLE Adenovirus vectors specific for cells expressing carcinoembryonic
antigens and methods of use thereof
JOURNAL Patent: JP 2002514075-A 1 14-MAY-2002;
CALYDON INC
COMMENT OS Unidentified
PN JP 2002514075-A/1
PD 14-MAY-2002
PF 03-MAR-1998 JP 1998538697
PR 03-MAR-1997 US 60/039763,02-MAR-1998 US 60/039763 PI
HENRY G LAMPARSKI,DANIEL R HENDERSON,ERIC R SCHUUR PC
C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12Q1/70,C12N11/08 CC
Strandedness: Double;
CC Topology: Linear;
CC Adenovirus vectors specific for cells expressing CC
carcinoembryonic antigens
CC and methods of use thereof
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RESULT 3
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DEFINITION Sequence 7 from patent US 6676935.
ACCESSION AR451687
VERSION AR451687.1 GI:42682802
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 472)
AUTHORS Henderson,D.R. and Schuur,E.R.
TITLE Tissue specific adenoviral vectors
JOURNAL Patent: US 6676935-A 7 13-JAN-2004;
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DEFINITION Sequence 54 from patent US 6676935.
ACCESSION AR451733
VERSION AR451733.1 GI:42682848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 472)
AUTHORS Henderson,D.R. and Schuur,E.R.
TITLE Tissue specific adenoviral vectors
JOURNAL Patent: US 6676935-A 54 13-JAN-2004;
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LOCUS AX705342 3500 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 11 from Patent WO03014388.
ACCESSION AX705342
VERSION AX705342.1 GI:29562007
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Distler,J., Model,F. and Taubert,H.
TITLE Method and nucleic acids for the analysis of colon cancer
JOURNAL Patent: WO 03014388-A 11 20-FEB-2003;
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DEFINITION Sequence 1 from patent US 6194211.
ACCESSION AR134885
VERSION AR134885.1 GI:14123790
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 11288)
TITLE        Richards,C.Ann. and Huber,B.
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JOURNAL      Patent: US 6194211-A 1 27-FEB-2001;
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VERSION    AR182304.1 GI:20225220
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11288)
AUTHORS    Huber,B. and Richards,C.A.
TITLE      Molecular constructs containing a carcinoembryonic antigen
JOURNAL    Patent: US 6337209-A 4 08-JAN-2002;
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Best Local Similarity 100.0%; Pred. No. 1.9e-142;
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KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11288)
AUTHORS    Huber,B. and Richards,C.A.
TITLE      Molecular constructs containing a carcinoembryonic antigen
JOURNAL    Patent: US 6337209-A 4 08-JAN-2002;
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Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 10414 TTTCTCTGTCAAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGACAGACACAG 10473
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QY 421 GCAGACCAAGAGTCTGAGGAACTGAAATAGAGGGGAAAAAGAGAGGGACAAAGA 471
DB 10714 GCAGACCAAGAGTCTGAGGAACTGAAATAGAGGGGAAAAAGAGAGGGACAAAGA 10764

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LOCUS      AR370519
DEFINITION Sequence 4 from patent US 6300490.
ACCESSION AR370519
VERSION    AR370519.1 GI:34607246
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11288)
AUTHORS    Huber,B., Richards,C.A. and Austin,E.A.
TITLE      Molecular constructs comprising a carcinoembryonic antigen (CEA)
JOURNAL    Patent: US 6300490-A 4 09-OCT-2001;
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VERSION AR479027.1 GI:47237926							
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SOURCE Unknown.							
ORGANISM Unknown.							
Unclassified.							
REFERENCE 1 (bases 1 to 11288)							
AUTHORS Huber,B. and Richards,C.A.							
TITLE Molecular constructs with a carcinoembryonic antigen (CEA)							
JOURNAL transcriptional regulatory sequence							
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Qy	61	GGCA	TCA	TCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG	120		
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Qy	241	GCCG	AAAGATT	TGCT	CTGAGGAACTCAAAATAGAGGGAAGAAAGGNGGGACAAAGA	300	
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Qy	301	GGCAG	AAATGAGAGGGGAGGGGACAGAGGACACCTGAAATAAAGACACACCCATGACCCA	360			
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DEFINITION	Sequence 1 from Patent WO0174861.		linear
ACCESSION	AX269130		
VERSION	AX269130.1	GI:16542049	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Vale,R.G., Harrington,K., Murphy,S. and Bateman,A.		
JOURNAL	Compositions and methods for tissue specific gene regulation		
FEATURES	therapy		
source	Patent: WO 0174861-A 1 11-OCT-2001;		
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Qy	181	CAGAGGTCAGCACTGGGGAAGACAGGTGTCTCTCCAGGGGATGGGGTCCATCCACCTT	240
Db	10474	CAGAGGTCAGCACTGGGGAAGACAGGTGTCTCTCCAGGGGATGGGGTCCATCCACCTT	10533
Qy	241	GCCGAAAAGATTGTTCTGAGGAACCTGAAATAGAGGGGAAAAAGAGGGGACAAAAGA	300
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Qy	301	GGCAGAAATCAGAGGGGGGGGACAGACACCTGMAATAAGACCCACCCATGACCCA	360
Db	10594	GGCAGAAATCAGAGGGGGGGGACAGACACCTGMAATAAGACCCACCCATGACCCA	10653
Qy	361	CGTGATGCTCAGAAGTACTCTCTGCCCTAGGAAAGACTCAGGGCAGAGGGAGGACCA	420
Db	10654	CGTGATGCTCAGAAGTACTCTCTGCCCTAGGAAAGACTCAGGGCAGAGGGAGGACCA	10713
Qy	421	GCAGACAGACAGCTCACAGACGCTTGACAAAACGTTCTCTGAACTCAAGC	471
Db	10714	GCAGACAGACAGCTCACAGACGCTTGACAAAACGTTCTCTGAACTCAAGC	10764

PR 03-MAR-1997 US 60/039763,02-MAR-1998 US 60/039763 PI
HENRY G LAMPARSKI,DANIEL R HENDERSON,ERIC R SCHUR PC
C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12Q1/70,C12N11/08 CC
Strandedness: Single;
CC Topology: linear;
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carcinoembryonic antigens
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LOCUS Adenovirus vectors containing cell status-specific response
DEFINITION elements and methods of use thereof.
ACCESSION BD224258
VERSION BD224258.1 GI:33034028
KEYWORDS JP 2002525063-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Yu, D.C. and Henderson, D.R.
REFERENCE 1 (bases 1 to 15056)
AUTHORS Adenovirus vectors containing cell status-specific response
elements and methods of use thereof
TITLE Patent: JP 2002525063-A 4 13-AUG-2002;
JOURNAL CALYDON INC

OS Homo sapiens (human)
PN JP 2002525063-A/4
PD 13-AUG-2002
PF 10-SEP-1999 JP 2000570347
PR 10-SEP-1998 US 60/099791,09-SEP-1999 US 09/392822 PI
DE CHAO YU,DANIEL R HENDERSON
PC C12N15/09,A61K48/00,A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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Best Local Similarity 100.0%; Pred. No. 2e-142;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 14362 GGCAGAAATGAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 361 CGTGATCTGAGAAGTACTCTGCTGCTAGGAAGACTCAGGCGAGAGGAGGAGGAGGAGG 420
Db 14422 CGTGATCTGAGAAGTACTCTGCTGCTAGGAAGACTCAGGCGAGAGGAGGAGGAGGAGG 14481
QY 421 GCAGACGACAGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 471
Db 14482 GCAGACGACAGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 14532

RESULT 14
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LOCUS Adenovirus vectors containing cell status-specific response
DEFINITION elements and methods of use thereof.
ACCESSION AR266427
VERSION AR266427.1 GI:29695383
KEYWORDS JP 2002525063-A/4.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15056)
AUTHORS Henderson, D.R. and Yu, D.C.
TITLE Target cell-specific adenoviral vectors containing E3 and methods

of use thereof
JOURNAL Patent: US 6495130-A 10 17-DEC-2002;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2e-142;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACCCACCTGAGCCTTTTCTAGCCCCCAGAGCCCTCTGTCACCTTCTCTGTTG 60
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QY 361 CGTGATGCTGAGAAAGTACTCTCTGCTTAGGAAGAGACTCAGGGCAGAGGGGAGGAAGGACA 420
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DEFINITION Sequence 14 from patent US 6692736.
ACCESSION AR474484
VERSION AR474484.1 GI:42713365
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15056)
AUTHORS Yu,D.-C., Li,Y., Little,A.S. and Henderson,D.R.
TITLE Cell-specific adenovirus vectors comprising an internal ribosome entry site
JOURNAL Patent: US 6692736-A 14 17-FEB-2004;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2e-142;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
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Perfect score: 472

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Searched: 4134886 seqs, 2624710521 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	471	99.8	15056	3	Aaa46851 Nucleotid
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11	471	99.8	15056	5	Aaf87238 CEA-TRE f
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ALIGNMENTS

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ID AAV52944 standard; DNA; 472 BP.

AC AAV52944;

XX 21-DEC-1998 (first entry)

XX CEA transcriptional regulatory element (CEA-TRE).

XX Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE;
KW human; promoter; enhancer; adenovirus; vector; cancer; gene therapy; ds.
XX Homo sapiens.
XX WO9839467-A2.
XX PD 11-SEP-1998.
XX PF 03-MAR-1998; 98WO-US004133.
XX PR 03-MAR-1997; 97US-0039763P.
XX PR 02-MAR-1998; 98US-00033555.
XX (CALY-) CALYDON INC.
XX Lamparski HG, Henerson DR, Schuur ER;
XX WPI; 1998-495862/42.
XX New adenovirus vectors, particularly for cancer therapy - comprising
PT adenovirus gene under transcriptional control of carcinoembryonic antigen
PT transcriptional regulatory element.
XX Claim 13; Page 62-63; 95pp; English.
XX This 472 nucleotide fragment comprises nucleotides -402 to +69 of the
CC human carcinoembryonic antigen transcriptional regulatory element (CEA-
CC TRE). It was isolated from human genomic DNA by PCR (see AAV52945-46).
CC The CEA-TRE is capable of mediating gene expression specific to cells
CC capable of expressing CEA or capable of CRE-TRE-mediated transcription. A
CC claimed replication-competent adenovirus (Ad) vector comprises an Ad gene
CC under transcriptional control of a CEA-TRE. Also claimed are: (1) a host
CC cell transformed with a Ad vector as above; (2) a method of making a

CC masked Ad, and (3) an Ad complexed with a masking agent. By providing for
CC transcripional initiating regulation dependent upon CEA expression,
CC virus replication can be restricted to target cells which allow a CEA-TRE
CC to function, particularly carcinoma cells expressing CEA. The vectors can
CC be used to detect and monitor samples for the presence of cells that
CC allow a CEA-TRE to function, and to selectively kill such cells,
CC especially malignant cells. Preferred vectors contain a CEA-TRE
CC comprising nucleotide 313-472 or 104-472 of the 472 nucleotide fragment,
CC especially comprising an enhancer and/or a promoter of the CEA gene
XX
SQ Sequence 472 BP; 142 A; 125 C; 134 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 472; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.6e-126; Indels 0; Gaps 0;
Matches 472; Conservative 0; Mismatches 0;
QY 1 AGCCACCCAGTGAAGCTTTTCTAGCCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG 60
DB 1 AGCCACCCAGTGAAGCTTTTCTAGCCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG 60
QY 61 GGCATATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGAGACCTGCTGGG 120
DB 61 GGCATATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGAGACCTGCTGGG 120
QY 121 TTTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
DB 121 TTTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
QY 181 CAGAGTTCAGCTAGTGGGAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
DB 181 CAGAGTTCAGCTAGTGGGAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
QY 241 GCGGAAAGATTGTCTGAGGAATCTGAAATAGAGGGAAGGAAAGAGGAGGACAAAGA 300
DB 241 GCGGAAAGATTGTCTGAGGAATCTGAAATAGAGGGAAGGAAAGAGGAGGACAAAGA 300
QY 301 GGCAGAAATGAGAGGGGGGAGACAGACACCTGAAATAGAGACACACACCTATGACCCA 360
DB 301 GGCAGAAATGAGAGGGGGGAGACAGACACCTGAAATAGAGACACACACCTATGACCCA 360
QY 361 CGTGATGCTGAGAAGTACTCTGCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGCA 420
DB 361 CGTGATGCTGAGAAGTACTCTGCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGCA 420
QY 421 GCAGACACAGCTACACAGGCTTGACAAAACGTTCTGGAATCAAGCA 472
DB 421 GCAGACACAGCTACACAGGCTTGACAAAACGTTCTGGAATCAAGCA 472

RESULT 2
ADI36414 standard; DNA; 472 BP.
AC ADI36414;
XX
XX
DT 22-APR-2004 (first entry)
XX
DE Human carcinoembryonic antigen transposon response element DNA SeqID7.
XX
XX ds; carcinoembryonic antigen; CEA; human; prostate;
KW transcripional response element; TRE; polyethylene glycol; PEG;
KW masking agent; tumour cell growth; proliferation; psoriatic lesion;
KW wound healing; hyperplasia; cancer; cytostatic; antipsoriatic; vulnerary.
XX
OS Homo sapiens.
XX
XX US2003152553-A1.
XX
XX 14-AUG-2003.
PD
XX
XX 02-MAY-2002; 2002US-00139089.
PF
XX
XX 27-JUN-1995; 95US-00495034.
PR

PR 26-JUN-1996; 96US-00669753.
PR 03-MAR-1997; 97US-0039597P.
PR 03-MAR-1997; 97US-0039762P.
PR 03-MAR-1997; 97US-0039763P.
PR 02-MAR-1998; 98US-00033333.
PR 02-MAR-1998; 98US-00033428.
PR 02-MAR-1998; 98US-00033555.
PR 10-SEP-1998; 98US-00051376.
PR 02-JUN-2000; 2000US-00509591.
XX
XX (LITT/) LITTLE A S.
PA (LAMP/) LAMPARSKI H G.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUR E R.
XX
XX Little AS, Lamparski HG, Henderson DR, Schuur ER;
WPI; 2004-119002/12.
XX
XX Composition comprising replication competent adenovirus having adenovirus
PT gene essential for replication under transcriptional control of cell type
PT specific transcriptional response element and masking agent.
XX
XX Disclosure; SEQ ID NO 7; 115pp; English.
XX
XX This invention relates to a novel composition that contains a replication
CC competent adenovirus capable of transfecting target host cells.
CC Specifically, it comprises an adenoviral gene essential for replication
CC (E1A, E1B or E4), which is under the transcriptional control of a
CC prostate specific transcriptional response element (TRE) and polyethylene
CC glycol (PEG) as the masking agent. The present invention describes this
CC composition as useful for suppressing tumour cell growth and for lowering
CC the levels of tumour cell markers. It can also be used for introducing
CC transient expression other than tumours, such as psoriatic lesions and wound
CC healing. In addition, it is useful for detecting cells where a cell type-
CC specific TRE is functional in a biological sample and for treating
CC prostate-associated diseases such as hyperplasia and cancer. As such,
CC these compositions exhibit cytostatic, antipsoriatic and vulnerary
CC activities. This polynucleotide sequence is the human carcinoembryonic
CC antigen (CEA) TRE DNA of the invention. NOTE: This sequence is identical
CC to that given as SeqID 54.
XX
SQ Sequence 472 BP; 142 A; 125 C; 134 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 472; DB 12; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.6e-126;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACCCAGTGAAGCTTTTCTAGCCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG 60
DB 1 AGCCACCCAGTGAAGCTTTTCTAGCCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG 60
QY 61 GGCATATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGAGACCTGCTGGG 120
DB 61 GGCATATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGAGACCTGCTGGG 120
QY 121 TTTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
DB 121 TTTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
QY 181 CAGAGTTCAGCTAGTGGGAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
DB 181 CAGAGTTCAGCTAGTGGGAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
QY 241 GCGGAAAGATTGTCTGAGGAATCTGAAATAGAGGGAAGGAAAGAGGAGGACAAAGA 300
DB 241 GCGGAAAGATTGTCTGAGGAATCTGAAATAGAGGGAAGGAAAGAGGAGGACAAAGA 300
QY 301 GGCAGAAATGAGAGGGGGGAGACAGAGGACACCTGAAATAGAGACACACCTATGACCCA 360
DB 301 GGCAGAAATGAGAGGGGGGAGACAGAGGACACCTGAAATAGAGACACACCTATGACCCA 360

QY 361 CGTGATCTGAGAAAGTACTCTCTGCTAGGAAGAGACTCAGGGCAGAGGAGGAAGGACA 420
Db |||||
361 CGTGATCTGAGAAAGTACTCTCTGCTAGGAAGAGACTCAGGGCAGAGGAGGAAGGACA 420
QY 421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCTTGAACTCAAGCA 472
Db |||||
421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCTTGAACTCAAGCA 472

RESULT 3

ID ADI36390 standard; DNA; 472 BP.
XX
AC ADI36390;
XX
DT 22-APR-2004 (first entry)
XX
DE Human carcinoembryonic antigen (CEA) TRE DNA sequence SeqID 54.
XX
KW db; CEA; carcinoembryonic antigen; human; prostate;
KW transcriptional response element; TRE; polyethylene glycol; PEG;
KW masking agent; tumour cell growth; proliferation; psoriatic lesion;
KW wound healing; hyperplasia; cancer; cycostatic; antipsoriatic; vulnery.
XX
OS Homo sapiens.
XX
PN US2003152553-A1.
XX
PD 14-AUG-2003.
XX
PF 02-MAY-2002; 2002US-00139089.
XX
PR 27-JUN-1995; 95US-00495034.
PR 26-JUN-1996; 96US-00669753.
PR 03-MAR-1997; 97US-0039597P.
PR 03-MAR-1997; 97US-0039762P.
PR 03-MAR-1997; 97US-0039763P.
PR 02-MAR-1998; 98US-00033333.
PR 02-MAR-1998; 98US-00033428.
PR 02-MAR-1998; 98US-00033555.
PR 10-SEP-1998; 98US-00151376.
PR 02-JUN-2000; 2000US-00509591.
XX

(LITT/) LITTLE A S.
PA (LAMP/) LAMPARSKI H G.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.

XX Little AS, Lamparski HG, Henderson DR, Schuur ER;

XX WPI; 2004-119002/12.

XX Composition comprising replication competent adenovirus having adenovirus
PT gene essential for replication under transcriptional control of cell type
PT specific transcriptional response element and masking agent.

PS Example 4; SEQ ID NO 54; 115pp; English.

XX This invention relates to a novel composition that contains a replication
CC competent adenovirus capable of transfecting target host cells.
CC Specifically, it comprises an adenoviral gene essential for replication
CC (E1A, E1B or E4), which is under the transcriptional control of a
CC prostate specific transcriptional response element (TRE) and polyethylene
CC glycol (PEG) as the masking agent. The present invention describes this
CC composition as useful for suppressing tumour cell growth and for lowering
CC the levels of tumour cell markers. It can also be used for introducing
CC transient expression that may be involved in treating undesired
CC proliferations other than tumours, such as psoriatic lesions and wound
CC healing. In addition, it is useful for detecting cells where a cell type-
CC specific TRE is functional in a biological sample and for treating
CC prostate-associated diseases such as hyperplasia and cancer. As such,
CC these compositions exhibit cytostatic, antipsoriatic and vulnery
CC activities. This polynucleotide sequence is a human carcinoembryonic

CC antigen (CEA) TRE DNA sequence of the invention. NOTE: This sequence is
XX identical to that given as SeqID 7.

SQ Sequence 472 BP; 142 A; 125 C; 134 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 472; DB 12; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.6e-126;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCACCCAGTGAGCCCTTTTCTAGCCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG 60

Db |||||
1 AGCCACCACCCAGTGAGCCCTTTTCTAGCCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG 60

QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGAGACCTGCTGGG 120

Db |||||
61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGAGACCTGCTGGG 120

QY 121 TTTCTCTGTCAAAAAGGAAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180

Db |||||
121 TTTCTCTGTCAAAAAGGAAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180

QY 181 CAGAGTCTAGCAGCTGGGGAAGACAGTTTCTCTCCAGGGGATGGGGGTCCATCCACCTT 240

Db |||||
181 CAGAGTCTAGCAGCTGGGGAAGACAGTTTCTCTCCAGGGGATGGGGGTCCATCCACCTT 240

QY 241 GCCGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGAAGGAGGAGGACAAAAGA 300

Db |||||
241 GCCGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGAAGGAGGAGGACAAAAGA 300

QY 301 GGCAGAAATGAGAGGGGGGAGAGAGGACACCTGAAATAAAGACACACCCATGACCCA 360

Db |||||
301 GGCAGAAATGAGAGGGGGGAGAGAGGACACCTGAAATAAAGACACACCCATGACCCA 360

QY 361 CGTGATCTGAGAAGTACTCTCTGCTAGGAAGAGACTCAGGGCAGAGGAGGAAGGACA 420

Db |||||
361 CGTGATCTGAGAAGTACTCTCTGCTAGGAAGAGACTCAGGGCAGAGGAGGAAGGACA 420

QY 421 GCAGACCAGACAGTCACAGCAGCCTTTCACAAAACGTTCTCTGGAACCTCAAGCA 472

Db |||||
421 GCAGACCAGACAGTCACAGCAGCCTTTCACAAAACGTTCTCTGGAACCTCAAGCA 472

RESULT 4

ACF62762

ID ACF62762 standard; DNA; 3500 BP.

XX ACF62762;

XX 09-OCT-2003 (first entry)

XX Human CEA genomic DNA SEQ ID NO:11.

XX Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
KW progesterone receptor; pcna; CEA; cdc2; c-erbB2; methylation; CpG;
KW characterization; classification; diagnosis; differentiation;
KW colon cell proliferative disorder; gene; ds.

OS Homo sapiens.

XX WO2003014388-A2.

XX 20-FEB-2003.

XX 09-AUG-2002; 2002WO-BP008939.

XX 09-AUG-2001; 2001DE-01039283.

XX (EPIG-) EPIGENOMICS AG.

XX Distler J, Model F, Taubert H;

XX WPI; 2003-256600/25.

XX

CC gene expression specific to cells capable of expressing CEA or capable of
CC CRE-TRE-mediated transcription. A claimed replication-competent
CC adenovirus (Ad) vector comprises an Ad gene under transcriptional control
CC of a CEA-TRE. By providing for transcriptional initiating regulation
CC dependent upon CEA expression, virus replication can be restricted to
CC target cells which allow a CEA-TRE to function, particularly carcinoma
CC cells expressing CEA. The vectors can be used to detect and monitor
CC samples for the presence of cells that allow a CEA-TRE to function, and
CC to selectively kill such cells, especially malignant cells
XX

SQ Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

Query Match 99.8%; Score 471; DB 2; Length 15056;
Best Local Similarity 100.0%; Pred. No. 1.3e-125; Mismatches 0; Indels 0; Gaps 0;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACACCCAGTGAAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACACCTTCTCTGTG 60
DB 14062 AGCCACACCCAGTGAAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACACCTTCTCTGTG 14121
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTCTGCTGG 120
DB 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTCTGCTGG 14181
QY 121 TTTCTCTGTACAAAGGAAATATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
DB 14182 TTTCTCTGTACAAAGGAAATATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 14241
QY 181 CAGAGTCTAGCAGTCTGGGGAAGACAGGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
DB 14242 CAGAGTCTAGCAGTCTGGGGAAGACAGGTCTCTCCAGGGGATGGGGTCCATCCACCTT 14301
QY 241 GCCGAAAAGATTGTCTGAGAACTGAAAATAGAGGGGAAAAAGAGGGAGGACAAAAGA 300
DB 14302 GCCGAAAAGATTGTCTGAGAACTGAAAATAGAGGGGAAAAAGAGGGAGGACAAAAGA 14361
QY 301 GGCAGAAATGAGGGGGGAGGAGGACAGGACACCTGTAATAGAGCCACACCCATGACCA 360
DB 14362 GGCAGAAATGAGGGGGGAGGAGGAGGACAGGACACCTGTAATAGAGCCACACCCATGACCA 14421
QY 361 CGTGATGCTGAGAACTACTCTCTGCTAGGAAAGACTCAGGGCAGAGGGAGGAGGAGCA 420
DB 14422 CGTGATGCTGAGAACTACTCTCTGCTAGGAAAGACTCAGGGCAGAGGGAGGAGGAGCA 14481
QY 421 GCAGACACAGATCAGACAGCCTTGACAAAACGTTCTGGAACCTCAAGC 471
DB 14482 GCAGACACAGATCAGACAGCCTTGACAAAACGTTCTGGAACCTCAAGC 14532

RESULT 8
AAZ99933
ID AAZ99933 standard; DNA; 15056 BP.
XX AC
XX AAZ99933;
XX
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA sequence of comprising a carcinoembryonic antigen TRE.
XX
KW Carcinoembryonic antigen; adenoviral vector; adenovirus gene;
KW transcriptional regulatory element; TRE; transcriptional control;
KW adenoviral propagation; tumour; 88.
XX
OS Unidentified.
XX
XX WO200015820-A1.
XX
XX
PD 23-MAR-2000.
XX
PF 10-SEP-1999; 99WO-US020718.
XX
XX 10-SEP-1998; 98US-0099791P.
PR 09-SEP-1999; 99US-00392822.

XX (CALY-) CALYDON INC.
XX PA
XX Yu DC, Henderson DR;
XX
XX WPI; 2000-271456/23.
XX
XX Adenovirus vectors comprising cell-status specific response elements
XX useful in gene therapy protocols for the treatment of cancers.
XX
XX Disclosure; Fig 5A-I; 79pp; English.

XX The present sequence comprises a transcriptional regulatory element (TRE)
XX from a carcinoembryonic antigen gene. The TRE is used to produce an
XX adenoviral vector of the invention. The specification describes an
XX adenovirus vector which comprises an adenovirus gene under
XX transcriptional control of a cell status specific TRE. The TRE is
XX preferably one that is essential for adenoviral propagation. The
XX adenovirus vectors may be used for the treatment of a range of tumours
XX such as lung, stomach, breast, colon and rectum, and uterine and cervix
XX cancers
SQ Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

Query Match 99.8%; Score 471; DB 3; Length 15056;
Best Local Similarity 100.0%; Pred. No. 1.3e-125; Mismatches 0; Indels 0; Gaps 0;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACACCCAGTGAAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACACCTTCTCTGTG 60
DB 14062 AGCCACACCCAGTGAAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACACCTTCTCTGTG 14121
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTCTGCTGG 120
DB 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTCTGCTGG 14181
QY 121 TTTCTCTGTACAAAGGAAATATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
DB 14182 TTTCTCTGTACAAAGGAAATATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 14241
QY 181 CAGAGTCTAGCAGTCTGGGGAAGACAGGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
DB 14242 CAGAGTCTAGCAGTCTGGGGAAGACAGGTCTCTCCAGGGGATGGGGTCCATCCACCTT 14301
QY 241 GCCGAAAAGATTGTCTGAGAACTGAAAATAGAGGGGAAAAAGAGGGAGGACAAAAGA 300
DB 14302 GCCGAAAAGATTGTCTGAGAACTGAAAATAGAGGGGAAAAAGAGGGAGGACAAAAGA 14361
QY 301 GGCAGAAATGAGGGGGGAGGAGGAGGACAGGACACCTGTAATAGAGCCACACCCATGACCA 360
DB 14362 GGCAGAAATGAGGGGGGAGGAGGAGGAGGACAGGACACCTGTAATAGAGCCACACCCATGACCA 14421
QY 361 CGTGATGCTGAGAACTACTCTCTGCTAGGAAAGACTCAGGGCAGAGGGAGGAGGAGCA 420
DB 14422 CGTGATGCTGAGAACTACTCTCTGCTAGGAAAGACTCAGGGCAGAGGGAGGAGGAGCA 14481
QY 421 GCAGACACAGATCAGACAGCCTTGACAAAACGTTCTGGAACCTCAAGC 471
DB 14482 GCAGACACAGATCAGACAGCCTTGACAAAACGTTCTGGAACCTCAAGC 14532

RESULT 9
AAA46851
ID AAA46851 standard; DNA; 15056 BP.
XX AC
XX AAA46851;
XX
XX 03-OCT-2000 (first entry)
XX
XX Nucleotide sequence of a CEA-TRE.
DE
KW Adenoviral vector; adenoviral gene; E3 sequence; cancer;
KW target cell-specific transcriptional regulatory element; TRE;

selective cytotoxicity; cell growth; tumour growth; ss.

Homo sapiens.

WO200039319-A2.

06-JUL-2000.

30-DEC-1999; 99WO-US031249.

30-DEC-1998; 98US-0114262P.

29-DEC-1999; 99US-00474699.

(CALY-) CALYDON INC.

Henderson DR, Yu D;

WPI; 2000-452409/39.

New adenoviral vector for selective targeting of cancer cells, comprises an adenovirus gene under transcriptional control of a target cell-specific transcriptional regulatory element and an E3 sequence.

Disclosure; Fig 23; 138pp; English.

The specification describes an adenoviral vector which comprises an adenoviral gene under the transcriptional control of a target cell-specific transcriptional regulatory element (TRE) and an E3 sequence. The vectors are useful for exerting selective cytotoxicity and/or suppressing cell growth (including tumour growth). This is especially useful in treating cancer in which targeted cell killing is desirable. This is also useful for targeted cytotoxic effects in other, non-tumour cells, when selective destruction and/or suppression of these cells is desirable. The vectors can also be useful for detecting the presence of cells which permit function of a target cell-specific TRE in, for example, an appropriate biological (such as clinical) sample. The adenovirus vector(s) can optionally selectively produce one or more proteins of interest in a target cell by using a heterologous, i.e., non-adenoviral, TRE. The present sequence represents a CEA-TRE, which is used in the course of the invention

Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

Query Match 99.8%; Score 471; DB 3; Length 15056;
Best Local Similarity 100.0%; Pred. No. 1.3e-125;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGCCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACTGTGTCACTTCTCTGTTG 60
DB	14062	AGCCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACTGTGTCACTTCTCTGTTG 14121
QY	61	GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGCCCGGACCCCTGCTGGG 120
DB	14122	GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGCCCGGACCCCTGCTGGG 14181
QY	121	TTTCTCTGTACAAAGAAATAATCCCTGTGTGTGACAGACCCCAAGACAGACACAG 180
DB	14182	TTTCTCTGTACAAAGAAATAATCCCTGTGTGTGACAGACCCCAAGACAGACACAG 14241
QY	181	CAGAGTTCAGCACTGGGGAGACAGTGTGTCTCCAGGGGATGGGGGTCCATCCACCTT 240
DB	14242	CAGAGTTCAGCACTGGGGAGACAGTGTGTCTCCAGGGGATGGGGGTCCATCCACCTT 14301
QY	241	GCCGAAGAATTGTCTGAGGAATCAATAAGAGGGAAGAAAGAGGGAGGACAAAGA 300
DB	14302	GCCGAAGAATTGTCTGAGGAATCAATAAGAGGGAAGAAAGAGGGAGGACAAAGA 14361
QY	301	GGCAGAAATGAGAGGGAGGGAGACAGACACTGAATAAGACACACACCCATGACCCA 360
DB	14362	GGCAGAAATGAGAGGGAGGGAGACAGACACTGAATAAGACACACACCCATGACCCA 14421
QY	361	CGTGATGCTGAGAAGTACTCTCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGACA 420

Db 14422 CGTGATGCTGAGAAGTACTCTCTGCCCTAGGAAGAGACTCAGGGCAGAGGAGGACACA 14481

QY 421 GCAGACCCAGACAGTCACAGCAGCCTTGACAAAACGTTCTCTGAACTCAAGC 471

Db 14482 GCAGACCCAGACAGTCACAGCAGCCTTGACAAAACGTTCTCTGAACTCAAGC 14532

RESULT 10

AAH43620

ID AAH43620 standard; cDNA; 15056 BP.

XX AC AAH43620;

XX DT 07-JAN-2002 (first entry)

XX DE CEA-TRE.

XX KW Adenovirus; ADP; replication-competent; adenoviral vector; TRE; PCR; transcriptional regulatory element; mutation; deletion; IRES; primer; promoter; internal ribosome entry site; cytotoxic; cancer; bladder; amplify; polymerase chain reaction; alpha-fetoprotein; AFP; EMCV; encephalomyocarditis virus; vascular endothelial growth factor; VEGF; immunoglobulin heavy-chain binding protein; BiP; uroplakin II; PDGF; platelet derived growth factor; hypoxia responsive element; HRE; prostate-specific antigen; PSA; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT precursor_RNA 14466..15056
FT /*tag= a
FT /note= "Transcription start site"

XX PN WO200173093-A2.

XX PD 04-OCT-2001.

XX XX 21-MAR-2001; 2001WO-US009036.

XX XX 24-MAR-2000; 2000US-0192156P.

XX XX (CALY-) CALYDON INC.

XX XX Yu D, Li Y, Henderson DR;

XX XX WPI; 2001-639234/73.

XX PT Replication-competent adenoviral vector, useful e.g. for killing cancer cells, contains two genes linked by internal ribosome entry site and controlled by target-specific regulator.

XX PS Example; Page 117-125; 148pp; English.

XX CC The sequences given in AAH43607-22 represent sequences which may be used in the replication-competent adenoviral vector (A) of the invention. The vector contains two genes (G1, G2) that are co-transcribed as a single mRNA and under control of a heterologous, target cell-specific transcriptional regulatory element (TRE). G2 has a mutation in, or deletion of, its endogenous promoter and is controlled from an internal ribosome entry site (IRES). (A) has greater specificity for a target cell than a similar vector in which TRE is operably linked to a gene and which lacks an IRES. (A) are used to modify the genotype of target cells, optionally in vitro with subsequent return of altered cells to the host and where G2 is a cytotoxic gene, to confer selective cytotoxicity to target cells, especially for killing cancer cells. Also (A) are used for diagnosis and monitoring, e.g. detection of bladder cancer cells. The target cell-specific TRE ensures that (A) has better targeting specificity, with minimal replication in non-target cells, so a runaway infection is prevented but production of adenoviral proteins in target cells activates and/or stimulates the immune response against target cells producing such proteins. The use of an IRES (rather than two identical control elements) eliminates the risk of homologous recombination and may provide enough extra space for an additional

CC	(therapeutic) gene	
XX	Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;	
SQ		
	Query Match	99.8%; Score 471; DB 5; Length 15056;
	Best Local Similarity	100.0%; Pred. No. 1.3e-125;
	Matches 471; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AGCCACCCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG	60
DB	14062 AGCCACCCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG	14121
QY	61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGCCCGGGACCCCTGCTGGG	120
DB	14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGCCCGGGACCCCTGCTGGG	14181
QY	121 TTTCTCTGTACAAAGGAAATAATCTCCCTCTGTGTGACAGACCCCAAGGACACACACAG	180
DB	14182 TTTCTCTGTACAAAGGAAATAATCTCCCTCTGTGTGACAGACCCCAAGGACACACACAG	14241
QY	181 CAGAGTCTAGCTGGGGAAGACAGGTTGCTCTCCAGGGGATGGGGTCCATCCACCTT	240
DB	14242 CAGAGTCTAGCTGGGGAAGACAGGTTGCTCTCCAGGGGATGGGGTCCATCCACCTT	14301
QY	241 GCCGAAAGATTGTCTGAGGAACCTGAAATAGAGGAAAGGAAAGAGGGACAAAGA	300
DB	14302 GCCGAAAGATTGTCTGAGGAACCTGAAATAGAGGAAAGGAAAGAGGGACAAAGA	14361
QY	301 GGCAGAAATGAGAGGGGGGACAGAGGACACCTGAAATAAGACACACCCATGACCCA	360
DB	14362 GGCAGAAATGAGAGGGGGGACAGAGGACACCTGAAATAAGACACACCCATGACCCA	14421
QY	361 CTTGATGCTGAGAACTCTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA	420
DB	14422 CTTGATGCTGAGAACTCTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA	14481
QY	421 CGAGACCAGACGTACAGCAGCCCTTGACAAAACGTTCTCGAACTCAAGC	471
DB	14482 CGAGACCAGACGTACAGCAGCCCTTGACAAAACGTTCTCGAACTCAAGC	14532
RESULT 11		
AAF87238		
ID	AAF87238 standard; DNA; 15056 BP.	
XX		
AC	AAF87238;	
XX		
DT	26-MAR-2002 (first entry)	
XX		
DE	CEA-TRE fusion protein coding sequence.	
XX		
KW	Tumour growth suppression; adenovirus vector; antineoplastic agent;	
KW	transcriptional regulatory element; TRE; radiotherapy; bladder cancer;	
KW	prostate cancer; liver cancer; breast cancer; colon cancer; melanoma;	
KW	ovarian cancer; pancreatic cancer; lung cancer; brain cancer; therapy;	
KW	CEA-TRE; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200172341-A2.	
XX		
PD	04-OCT-2001.	
XX		
PF	21-MAR-2001; 2001WO-US009042.	
XX		
PR	24-MAR-2000; 2000US-0192015P.	
XX		
PA	(CALY-) CALYDON INC.	
XX		
PI	Yu D, Chen Y, Henderson DR;	
XX		
DR	WPI; 2001-648426/74.	
XX		
XX		

Suppression of tumor growth, e.g. liver, bladder or breast cancer, comprises using a synergistic combination of adenovirus vector and antineoplastic agent or radiotherapy.

Claim 12; Page 185-193; 248pp; English.

This sequence represents a CEA-TRE fusion protein coding sequence used in the scope of the invention. The invention relates to a method for the suppression of tumour growth comprising the administration of: (a) a target cell-specific adenovirus vector comprising an adenoviral gene essential for replication under transcriptional control of a target cell-specific transcriptional regulatory element (TRE); and (b) at least one antineoplastic agent; or (c) a course of radiotherapy where the amount of (a) and/or (b) or (c) is lower than that known to be effective for suppressing tumour growth when administered alone. The method is used for suppression of tumour growth for treatment of e.g. bladder cancer, prostate cancer, liver cancer, breast cancer, colon cancer, melanoma, ovarian cancer, pancreatic cancer, lung cancer or brain cancer. The combinations enhance the efficacy of treatment, allowing lower doses to be administered, reducing toxicity and suffering of the patient

Sequence 15056 BP; 3848 A; 4126 C; 4010 G; 3072 T; 0 U; 0 Other;

Query Match 99.8%; Score 471; DB 5; Length 15056;

Best Local Similarity 100.0%; Pred. No. 1.3e-125; Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG 60

DB 14062 AGCCACCCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG 14121

QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGCCCGGGACCCCTGCTGGG 120

DB 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGCCCGGGACCCCTGCTGGG 14181

QY 121 TTTCTCTGTACAAAGGAAATAATCTCCCTCTGTGTGACAGACCCCAAGGACACACACAG 180

DB 14182 TTTCTCTGTACAAAGGAAATAATCTCCCTCTGTGTGACAGACCCCAAGGACACACACAG 14241

QY 181 CAGAGTCTAGCTGGGGAAGACAGGTTGCTCTCCAGGGGATGGGGTCCATCCACCTT 240

DB 14242 CAGAGTCTAGCTGGGGAAGACAGGTTGCTCTCCAGGGGATGGGGTCCATCCACCTT 14301

QY 241 GCCGAAAGATTGTCTGAGGAACCTGAAATAGAGGAAAGGAAAGAGGGACAAAGA 300

DB 14302 GCCGAAAGATTGTCTGAGGAACCTGAAATAGAGGAAAGGAAAGAGGGACAAAGA 14361

QY 301 GGCAGAAATGAGAGGGGGGACAGAGGACACCTGAAATAAGACACACCCATGACCCA 360

DB 14362 GGCAGAAATGAGAGGGGGGACAGAGGACACCTGAAATAAGACACACCCATGACCCA 14421

QY 361 CTTGATGCTGAGAACTCTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420

DB 14422 CTTGATGCTGAGAACTCTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 14481

QY 421 CGAGACCAGACGTACAGCAGCCCTTGACAAAACGTTCTCGAACTCAAGC 471

DB 14482 CGAGACCAGACGTACAGCAGCCCTTGACAAAACGTTCTCGAACTCAAGC 14532

RESULT 12

ABK9582

ID ABK9582 standard; DNA; 15056 BP.

XX

AC ABK9582;

XX

DT 21-OCT-2002 (first entry)

XX

DE Prostate-specific antigen transcriptional regulatory element (TRE).

XX

KW Adenovirus; transcriptional regulatory element; TRE; prostate; liver;

KW breast cancer; colon cancer; antitumour; gene; ds; probasin; PB; human;

KW rat; carcinoembryonic antigen; prostate-specific antigen; ADP;

adenovirus death protein; glandular kallikrein.
Unidentified.

US2002068049-A1.

06-JUN-2002.

06-DEC-2000; 2000US-00732169.

10-SEP-1998; 98US-00151376.

(HEND/) HENDERSON D R.
(SCHU/) SCHUUR E R.

Henderson DR, Schuur ER;

WPI; 2002-582468/62.

Novel adenovirus vector comprises adenovirus gene under transcriptional control of cell-type specific transcriptional response element for conferring selective toxicity on target cell and for suppressing tumor growth.

Disclosure; Fig 15; 83pp; English.

The invention relates to an adenovirus vector (AV) comprising an AV gene under transcriptional control of a cell type-specific transcriptional regulatory element (TRE) and optionally a first AV gene under control of a first cell type-specific TRE and a second gene under control of a second cell type-specific TRE, where the first and second cell type-specific TREs are substantially identical. When the vector is introduced into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon cancer cell) it allows the cell type-specific TRE to function, resulting in cytotoxicity. The vector is useful for suppressing tumour growth of a target cell. This sequence represents a polynucleotide used in the scope of the invention

Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

Query Match 99.8%; Score 471; DB 6; Length 15056;

Best Local Similarity 100.0%; Pred. No. 1.3e-125;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTCTCACTTCTCTGTTG 60
DB 14062 AGCCACCCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTCTCACTTCTCTGTTG 14121
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTGCTGGG 120
DB 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTGCTGGG 14181
QY 121 TTTCTCTGTCAAAAGAAATATATCCCTGTGTGACAGACCCAGGACGAAACACAG 180
DB 14182 TTTCTCTGTCAAAAGAAATATATCCCTGTGTGACAGACCCAGGACGAAACACAG 14241
QY 181 CAGAGTTCAGCAGTGGGAGAGCAGTTGTCCTCCAGGGGATGGGGTCCATCCACCTT 240
DB 14242 CAGAGTTCAGCAGTGGGAGAGCAGTTGTCCTCCAGGGGATGGGGTCCATCCACCTT 14301
QY 241 GCCGAAAGATTGTCTGAGGAATGAAATAGAGGAAAAAGAGGGGACAAAGA 300
DB 14302 GCCGAAAGATTGTCTGAGGAATGAAATAGAGGAAAAAGAGGGGACAAAGA 14361
QY 301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACTGAATAAGACCAACCCATGACCCA 360
DB 14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACTGAATAAGACCAACCCATGACCCA 14421
QY 361 CGTGATGCTGAGAGTACTCTCTCCCTAGGAAGAGACTAGGCGAGAGGGAGGAGACA 420
DB 14422 CGTGATGCTGAGAGTACTCTCTCCCTAGGAAGAGACTAGGCGAGAGGGAGGAGACA 14481
QY 421 GCAGACCAGACAGTTCACAGCAGCCTTGACAAAAACGTTCTCTGGAACCTCAAGC 471

DB 14482 GCAGACCAGACAGTTCACAGCAGCCTTGACAAAACGTTCTCTGGAACCTCAAGC 14532

RESULT 13

ACD07309

XX ACD07309 standard; DNA; 15056 BP.

XX ACD07309;

XX 07-AUG-2003 (first entry)

XX Human carcinoembryonic antigen (CEA) TRE.

XX Adenoviral vector; adenovirus gene; transcriptional control; TRE;
XX cell type-specific; transcriptional response element; PSA; hKLUK;
XX prostate-specific antigen; glandular kallikrein; probastin; PB;
XX carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1;
XX cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic; human;
XX ds.

XX Homo sapiens.

XX US2003044383-A1.

XX 06-MAR-2003.

XX 10-SEP-1998; 98US-00151376.

XX 27-JUN-1995; 95US-00495034.

XX 20-AUG-1996; 96US-00699753.

XX 03-MAR-1997; 97US-0039597P.

XX 03-MAR-1997; 97US-0039599P.

XX 03-MAR-1997; 97US-0039762P.

XX 03-MAR-1997; 97US-0039763P.

XX 02-MAR-1998; 98US-00033333.

XX 02-MAR-1998; 98US-00033428.

XX 02-MAR-1998; 98US-00033555.

XX (HEND/) HENDERSON D R.

XX (SCHU/) SCHUUR E R.

XX Henderson DR, Schuur ER;

XX WPI; 2003-456547/43.

XX New adenovirus vector for transfecting target host cells, comprises an adenovirus gene under transcriptional control of a cell type-specific transcriptional response element.

XX Disclosure; Fig 14; 83pp; English.

XX The present invention relates to adenoviral vectors comprising an adenovirus gene under transcriptional control of a cell type-specific transcriptional response element (TRE). Example TREs given in the specification include human prostate-specific antigen (PSA) TRE, human glandular kallikrein (hKLUK) TRE, rat probastin (PB) TRE, human carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3 (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for introducing new genetic capability, particularly associated with cytotoxicity for treating neoplasia. For example, the vector may be used in a target cell to suppress tumour growth, or to kill the target cell. The vector is particularly useful in gene therapy. The present sequence represents a TRE

XX Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

Query Match 99.8%; Score 471; DB 8; Length 15056;

Best Local Similarity 100.0%; Pred. No. 1.3e-125;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCCAGTGGAGCCCTTTTCTAGCCCCAGAGCCACCTCTCTCACTTCTCTGTTG 60

Db 14062 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACACTTCTCTGTTG 14121
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGAGACCTCTCTGGG 120
Db 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGAGACCTCTCTGGG 14181
QY 121 TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGACAGACACAG 180
Db 14182 TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGACAGACACAG 14241
QY 181 CAGAGGTCTGAGGAGAGAGAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 14242 CAGAGGTCTGAGGAGAGAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 14301
QY 241 GCCGAAAGATTGTCTGAGGAACCTGAATAAGAGGGGAAAGAGAGGAGGACAAAGA 300
Db 14302 GCCGAAAGATTGTCTGAGGAACCTGAATAAGAGGGGAAAGAGAGGAGGACAAAGA 14361
QY 301 GGCAGAAATGAGGGGGGGGACAGAGGACACCTGAAATTAAGACACACCCATGACCA 360
Db 14362 GGCAGAAATGAGGGGGGGGACAGAGGACACCTGAAATTAAGACACACCCATGACCA 14421
QY 361 CGTGATGCTGAGAACTACTCTCTGCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db 14422 CGTGATGCTGAGAACTACTCTCTGCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 14481
QY 421 GCAGACCCAGACAGTCACAGACGCTTGACAAACCTTCTGGAATCAAGC 471
Db 14482 GCAGACCCAGACAGTCACAGACGCTTGACAAACCTTCTGGAATCAAGC 14532

RESULT 14
ADB54000
ID ADB54000 standard; DNA; 4138 BP.
XX
XX
XX ADB54000;
XX
XX
XX 04-DEC-2003 (first entry)
XX CEA genomic DNA region.
XX
KW colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
XX
OS Unidentified.
XX
PN WO2003072821-A2.
XX
XX
XX 04-SEP-2003.
XX
XX 27-FEB-2003; 2003WO-EP02035.
XX
XX 27-FEB-2002; 2002EP-00004551.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
PI Rujan T, Schmitt A;
XX
XX WPI; 2003-731620/69.
XX
XX
PT Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
XX Claim 46; SEQ ID NO 56; 74pp; English.
XX
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of

CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytostatic activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligoners are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the genomic DNA region of
CC the invention. This sequence is not shown within the specification but is
CC taken from Wipoweb.
XX
SQ Sequence 4138 BP; 1048 A; 1201 C; 1059 G; 830 T; 0 U; 0 Other;
Query Match 96.6%; Score 455.8; DB 10; Length 4138;
Best Local Similarity 99.4%; Pred. No. 1.9e-121;
Matches 468; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACACTTCTCTGTTG 60
Db 2109 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACACTTCTCTGTTG 2168
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGAGACCTCTCTGGG 120
Db 2169 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGAGACCTCTCTGGG 2228
QY 121 TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGACAGACACAG 180
Db 2229 TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGACAGACACAG 2288
QY 181 CAGAGGTCTGAGGAGAGAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 2289 CAGAGGTCTGAGGAGAGAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 2348
QY 241 GCCGAAAGATTGTCTGAGGAACCTGAATAAGAGGGGAAAGAGAGGAGGACAAAGA 300
Db 2349 GCCGAAAGATTGTCTGAGGAACCTGAATAAGAGGGGAAAGAGAGGAGGACAAAGA 2408
QY 301 GGCAGAAATGAGGGGGGGGACAGAGGACACCTGAAATTAAGACACACCCATGACCA 360
Db 2409 GGCAGAAATGAGGGGGGGGACAGAGGACACCTGAAATTAAGACACACCCATGACCA 2467
QY 361 CGTGATGCTGAGAACTACTCTCTGCTAGGAGAGACTCAGGGCAGAGGGAGGAGGAGACA 420
Db 2468 CGTGATGCTGAGAACTACTCTCTGCTAGGAGAGACTCAGGGCAGAGGGAGGAGGAGACA 2527
QY 421 GCAGACCCAGACAGTCACAGACGCTTGACAAACCTTCTGGAATCAAGC 471
Db 2528 GCAGACCCAGACAGTCACAGACGCTTGACAAACCTTCTGGAATCAAGC 2578
RESULT 15
ADC37109
ID ADC37109 standard; DNA; 3281 BP.
XX
XX
XX ADC37109;
XX
XX
XX 18-DEC-2003 (first entry)
XX
XX
XX DNA of a human carcinoembryonic antigen, CEA, gene.
XX
XX
XX DNA vaccine; immune response; carcinoembryonic antigen; CEA; CD40 ligand;
XX homotrimer; cytostatic; gene therapy; cancer; colon cancer; human; gene;
XX ds.
XX
XX Homo sapiens.
XX
XX WO2003074712-A1.
XX
XX
XX 12-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-US006295.
XX
XX 02-MAR-2002; 2002US-00090238.
XX


```

XX (SRI ) SCRIPPS RES INST.
XX
XX PI Xiang R, Reisfeld RA;
XX
XX DR WPI; 2003-748281/70.
XX
XX New DNA vaccine for eliciting an immune response against cells presenting
PT a carcinoembryonic antigen (CEA) such as colon cancer cells, comprises
PT plasmid DNAs encoding a CEA and/or a CD40 ligand, together with a
PT carrier.
XX
XX Disclosure; SEQ ID NO 1; 48pp; English.
XX
XX The invention relates to a novel DNA vaccine for eliciting an immune
CC response against cells that present a carcinoembryonic antigen (CEA). The
CC vaccine comprises a plasmid DNA operably encoding a CEA, and a plasmid
CC DNA operably encoding a CD40 ligand or its homotrimer, together with a
CC carrier. The DNA vaccine has cytostatic activity and may be used in gene
CC therapy to treat disorders. The DNA vaccine is useful in preventing
CC cancers, such as colon cancer, by eliciting an immune response against
CC cells that present CEA, including colon cancer cells. This polynucleotide
CC sequence represents the DNA of a human CEA gene, used as a ligand of the
XX invention.
XX
XX Sequence 3281 BP; 847 A; 953 C; 871 G; 610 T; 0 U; 0 Other;
XX
Query Match 31.6%; Score 432.4; DB 10; Length 3281;
Best Local Similarity 98.9%; Pred. No. 1.1e-114;
Matches 467; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
QY 1 AGCCACACCCAGTGGAGCCCTTTTCTAGCCCCCAGAGCCACCTCTGTCACTTCTCTGTG 60
DB 1261 AGCCACACCCAGTGGAGCCCTTTTCTAGCCCCCAGAGCCACCTCTGTCACTTCTCTGTG 1320
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 120
DB 1321 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCGGGACCC 1379
QY 121 TTTCTCTGTACAAAGGAAATATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
DB 1380 TTTCTCTGTACAAAGGAAATATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 1439
QY 181 CAGAGGTCAGCAGTGGGG--AAGACAGTTGTCTCTCCAGGGATGGGGTCCATCCACCT 239
DB 1440 CAGAGGTCAGCAGTGGGGAAAGCAGGTTGTC--CAGAGGGATGGGGTCCATCCACCT 1497
QY 240 TGCCGAAAGATTGTCTGAGGAACCTGAAAATAGAAAGGAAAGAGAGGGGACAAAAG 299
DB 1498 TGCCGAAAGATTGTCTGAGGAACCTGAAAATAGAAAGGAAAGAGAGGGGACAAAAG 1557
QY 300 AGGCAGAAATGAGAGGGAGGGGACAGAGACACCTGAAATAAAGACACACCCATGACCC 359
DB 1558 AGGCAGAAATGAGAGGGAGGGGACAGAGACACCTGAAATAAAGACACACCCATGACCC 1617
QY 360 ACCTGATGCTGAGAAGTACTCTGCTAGGAGAGACTCAGGGCAGAGGAGGAGGAC 419
DB 1618 ACCTGATGCTGAGAAGTACTCTGCTAGGAGAGACTCAGGGCAGAGGAGGAGGAGGAC 1677
QY 420 AGCAGACCACAGAGTCACAGCAGCCTTGACAAAACGTTCTCTGGAATCAAGC 471
DB 1678 AGCAGACCACAGAGTCACAGCAGCCTTGACAAAACGTTCTCTGGAATCAAGC 1729

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OM nucleic - nucleic search, using sw model

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	472	100.0	472	4	US-09-151-376-7
3	472	100.0	472	4	US-09-151-376-54
4	471	99.8	11288	3	US-08-646-301A-1
5	471	99.8	11288	3	US-08-481-968A-4
6	471	99.8	11288	3	US-08-154-712B-4
7	471	99.8	11288	4	US-09-947-923A-4
8	471	99.8	15056	4	US-09-474-699-10
9	471	99.8	15056	4	US-09-814-351-14
10	156.6	33.2	2073	4	US-09-924-103-1
11	94	19.9	3774	3	US-08-646-301A-2
12	94	19.9	3774	3	US-08-481-968A-5
13	94	19.9	3774	3	US-08-154-712B-5
14	94	19.9	3774	4	US-09-947-923A-5
15	71.2	15.1	7218	1	US-08-232-463-14
16	57.6	12.2	387	4	US-09-370-838-177
17	57.6	12.2	387	4	US-09-854-133-177
18	57.2	12.1	460	4	US-09-401-064-169
19	56.4	11.9	319	4	US-09-513-999C-14905
20	54.8	11.6	306	4	US-09-513-999C-14903
21	54.8	11.6	327	4	US-09-513-999C-14902
22	54.8	11.6	414	4	US-09-513-999C-14904
23	54.6	11.6	504	4	US-09-513-999C-14906
24	54.2	11.5	502	4	US-09-513-999C-8661
25	54.2	11.5	2115	4	US-09-513-999C-14901
26	54	11.4	2220	1	US-08-389-459A-16
27	54	11.4	2220	3	US-08-987-867A-16

28	53.4	11.3	525	4	US-09-513-999C-3741	Sequence 3741, Ap
c 29	44.2	9.4	319	3	US-09-385-982-486	Sequence 486, App
c 30	40.4	8.6	505	4	US-09-621-976-15639	Sequence 15639, A
31	39.2	8.3	289	3	US-09-007-005-17	Sequence 17, Appl
32	39.2	8.3	289	3	US-09-244-796-17	Sequence 17, Appl
33	38	8.1	7898	3	US-08-984-709A-49	Sequence 49, Appl
34	37.6	8.0	439	4	US-09-513-999C-14899	Sequence 14899, A
35	37	7.8	1413	3	US-08-984-709A-52	Sequence 52, Appl
36	36.2	7.7	432	4	US-09-513-999C-8272	Sequence 8272, Ap
37	35.6	7.5	50	1	US-08-171-389-332	Sequence 392, App
38	35.6	7.5	50	1	US-08-123-936-392	Sequence 392, App
39	35.6	7.5	50	2	US-08-475-228A-392	Sequence 392, App
40	35.6	7.5	50	3	US-08-482-080A-392	Sequence 392, App
41	35.6	7.5	50	3	US-09-354-947-392	Sequence 392, App
42	35.6	7.5	50	5	PCT-US93-12388-392	Sequence 392, App
c 43	35.6	7.5	545	4	US-09-270-767-2655	Sequence 2655, Ap
c 44	35.6	7.5	545	4	US-09-270-767-17937	Sequence 17937, A
c 45	34.2	7.2	335	4	US-09-621-976-13385	Sequence 13385, A

ALIGNMENTS

RESULT 1

US-09-033-556-7
; Sequence 7, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; OF USING SAME
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-033-556-7

Query Match 100.0%; Score 472; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 9.2e-134;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 AGCCACCCAGTGGAGGCTTTTCTAGCCCCAGAGCCACTCTGTCAACCTTCTCTGTG 60
Db |||||
Oy 1 AGCCACCCAGTGGAGGCTTTTCTAGCCCCAGAGCCACTCTGTCAACCTTCTCTGTG 60
Db |||||
Oy 61 GGCATCATCCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTTCTGGG 120
Db |||||
Oy 61 GGCATCATCCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTTCTGGG 120
Db |||||
Oy 121 TTTCTCTGTCAAAAGGAAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACAG 180
Db |||||
Oy 121 TTTCTCTGTCAAAAGGAAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACAG 180
Db |||||
Oy 181 CAGAGGTGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db |||||
Oy 181 CAGAGGTGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db |||||
Oy 241 GCGGAAAAGATTGTCTGAGGAATCTGAAAATAGAAAGGAAAAGAGGAGGACAAAAGA 300
Db |||||
Oy 241 GCGGAAAAGATTGTCTGAGGAATCTGAAAATAGAAAGGAAAAGAGGAGGACAAAAGA 300
Db |||||
Oy 301 GGCAGAAATAGAGGGGAGGAGAGAGGAGACCTGAAATAAGACCAACCCATGACCCA 360
Db |||||
Oy 301 GGCAGAAATAGAGGGGAGGAGAGAGGAGACCTGAAATAAGACCAACCCATGACCCA 360
Db |||||
Oy 361 CGTGATGCTGAGAGTACTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db |||||
Oy 361 CGTGATGCTGAGAGTACTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db |||||
Oy 421 GCAGACCAAGAGTCTGAGGAGCTTGCACAGCCCTTGACAAAACGTTCTGGAACCTCAAGCA 472
Db |||||
Oy 421 GCAGACCAAGAGTCTGAGGAGCTTGCACAGCCCTTGACAAAACGTTCTGGAACCTCAAGCA 472
Db |||||
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RESULT 2

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US-09-151-376-7
; Sequence 7, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 34802200221
; CURRENT APPLICATION NUMBER: US/09/151,376
; EARLIER FILING DATE: 1998-09-10
; EARLIER FILING DATE: 1996-06-26
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-151-376-7
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Query Match 100.0%; Score 472; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 9.2e-134;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 AGCCACCCAGTGGAGGCTTTTCTAGCCCCAGAGCCACTCTGTCAACCTTCTCTGTG 60
Db |||||
Oy 1 AGCCACCCAGTGGAGGCTTTTCTAGCCCCAGAGCCACTCTGTCAACCTTCTCTGTG 60
Db |||||
Oy 61 GGCATCATCCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTTCTGGG 120
Db |||||
Oy 61 GGCATCATCCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTTCTGGG 120
Db |||||
Oy 121 TTTCTCTGTCAAAAGGAAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACAG 180
Db |||||
Oy 121 TTTCTCTGTCAAAAGGAAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACAG 180
Db |||||
Oy 181 CAGAGGTGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db |||||
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Db |||||
Oy 181 CAGAGGTGAGGAGGCTTTTCTAGCCCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db |||||
Oy 241 GCGGAAAAGATTGTCTGAGGAATCTGAAAATAGAAAGGAAAAGAGGAGGACAAAAGA 300
Db |||||
Oy 241 GCGGAAAAGATTGTCTGAGGAATCTGAAAATAGAAAGGAAAAGAGGAGGACAAAAGA 300
Db |||||
Oy 301 GGCAGAAATAGAGGGGAGGAGAGGAGACCTGAAATAAGACCAACCCATGACCCA 360
Db |||||
Oy 301 GGCAGAAATAGAGGGGAGGAGAGGAGACCTGAAATAAGACCAACCCATGACCCA 360
Db |||||
Oy 361 CGTGATGCTGAGAGTACTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db |||||
Oy 361 CGTGATGCTGAGAGTACTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db |||||
Oy 421 GCAGACCAAGAGTCTGAGGAGCTTGCACAGCCCTTGACAAAACGTTCTGGAACCTCAAGCA 472
Db |||||
Oy 421 GCAGACCAAGAGTCTGAGGAGCTTGCACAGCCCTTGACAAAACGTTCTGGAACCTCAAGCA 472
Db |||||
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RESULT 3

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US-09-151-376-54
; Sequence 54, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 34802200221
; CURRENT APPLICATION NUMBER: US/09/151,376
; EARLIER FILING DATE: 1998-09-10
; EARLIER FILING DATE: 1996-06-26
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-151-376-54
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Query Match 100.0%; Score 472; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 9.2e-134;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 AGCCACCCAGTGGAGGCTTTTCTAGCCCCAGAGCCACTCTGTCAACCTTCTCTGTG 60
Db |||||
Oy 1 AGCCACCCAGTGGAGGCTTTTCTAGCCCCAGAGCCACTCTGTCAACCTTCTCTGTG 60
Db |||||
Oy 61 GGCATCATCCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTTCTGGG 120
Db |||||
Oy 61 GGCATCATCCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTTCTGGG 120
Db |||||
Oy 121 TTTCTCTGTCAAAAGGAAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACAG 180
Db |||||
Oy 121 TTTCTCTGTCAAAAGGAAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACAG 180
Db |||||
Oy 181 CAGAGGTGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db |||||
Oy 181 CAGAGGTGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db |||||
Oy 241 GCGGAAAAGATTGTCTGAGGAATCTGAAAATAGAAAGGAAAAGAGGAGGACAAAAGA 300
Db |||||
Oy 241 GCGGAAAAGATTGTCTGAGGAATCTGAAAATAGAAAGGAAAAGAGGAGGACAAAAGA 300
Db |||||
Oy 301 GGCAGAAATAGAGGGGAGGAGAGGAGACCTGAAATAAGACCAACCCATGACCCA 360
Db |||||
Oy 301 GGCAGAAATAGAGGGGAGGAGAGGAGACCTGAAATAAGACCAACCCATGACCCA 360
Db |||||
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Qy	361	CGTGATGCTCAGAAAGTACTCTCTCCCTAGAAAGAGACTCAGGGCAGAGGGAGGAGACA	420
Db	361	CGTGATGCTCAGAAAGTACTCTCTCCCTAGAAAGAGACTCAGGGCAGAGGGAGGAGACA	420
Qy	421	GCAGACCAGACAGCTCAACGAGCGCTTTGACAAAACGTTCTCTGGAACTCAAGCA	472
Db	421	GCAGACCAGACAGCTCAACGAGCGCTTTGACAAAACGTTCTCTGGAACTCAAGCA	472

RESULT 4
 US-08-646-301A-1
 ; Sequence 1, Application US/08646301A
 ; Patent No. 6194211
 ; GENERAL INFORMATION:
 ; APPLICANT: Richards, Cynthia Ann
 ; APPLICANT: Huber, Brian E.
 ; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
 ; Patent No. 6194211
 ; TITLE OF INVENTION: Antigen for Expression Targeting
 ; FILE REFERENCE: PBI50805W
 ; CURRENT APPLICATION NUMBER: US/08/646,301A
 ; CURRENT FILING DATE: 1996-05-16
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 11288
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-08-646-301A-1

Query Match	99.9%	Score	471	DB 3	Length	11288							
Best Local Similarity	100.0%	Pred. No.	8.4e-133										
Matches	471	Conservative	0	Mismatches	0	Gaps	0						
Qy	1	AGCCACCA	CCAGT	GTAGCC	TTTTTCT	TAGCCCCC	CAGAGCCACCTCTGT	CACCTTCTCTGT	60				
Db	10294	AGCCACCA	CCAGT	GTAGCC	TTTTTCT	TAGCCCCC	CAGAGCCACCTCTGT	CACCTTCTCTGT	10353				
Qy	61	GGCANTAT	CCAC	CTTCC	CMAG	AGCCCT	TGGAGAGCAT	TGGGGAGACCCGGG	ACCTCTCTGGG	120			
Db	10354	GGCANTAT	CCAC	CTTCC	CMAG	AGCCCT	TGGAGAGCAT	TGGGGAGACCCGGG	ACCTCTCTGGG	10413			
Qy	121	TTTCTCTG	TACAA	AGGAA	TAAT	ATAT	CCCTCT	GTGTGACAGAC	CCAAAGGACAGACACAG	180			
Db	10414	TTTCTCTG	TACAA	AGGAA	TAAT	ATAT	CCCTCT	GTGTGACAGAC	CCAAAGGACAGACACAG	10473			
Qy	181	CAGAGT	TCAGCA	CTGGGG	AAAG	CAG	GTTF	GTCTCC	CAGGGGATGGGG	GTCCATTCACCTTT	240		
Db	10474	CAGAGT	TCAGCA	CTGGGG	AAAG	CAG	GTTF	GTCTCC	CAGGGGATGGGG	GTCCATTCACCTTT	10533		
Qy	241	GCCGAA	GAATTT	TGCT	GTAG	GA	ACTG	CAAA	TAGA	GGGAAAAAAGAGGAGGGACAAAAGA	300		
Db	10534	GCCGAA	GAATTT	TGCT	GTAG	GA	ACTG	CAAA	TAGA	GGGAAAAAAGAGGAGGGACAAAAGA	10593		
Qy	301	GGCAGAA	TATCAG	AGGGG	AGGGG	CAG	AGGAC	CACTT	GAA	TAAAGACCA	CCCATGCCCA	360	
Db	10594	GGCAGAA	TATCAG	AGGGG	AGGGG	CAG	AGGAC	CACTT	GAA	TAAAGACCA	CCCATGCCCA	10653	
Qy	361	CGTGAT	CTCAG	AA	GTACT	CTCT	CGCCCT	TAGG	AGAG	ACTCAG	GGGCGAGGGAGGAGGACA	420	
Db	10654	CGTGAT	CTCAG	AA	GTACT	CTCT	CGCCCT	TAGG	AGAG	ACTCAG	GGGCGAGGGAGGAGGACA	10713	
Qy	421	GCAGAC	CCAG	CAGT	CA	CAG	CAG	CTTT	GC	AAAA	CGTTCTCTG	GAACCTCAAGC	471
Db	10714	GCAGAC	CCAG	CAGT	CA	CAG	CAG	CTTT	GC	AAAA	CGTTCTCTG	GAACCTCAAGC	10764

RESULT 5
US-08-481-968A-4
; Sequence 4, Application US/08481968A
; Patent No. 6300490
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian

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; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA)
; TITLE OF INVENTION: Transcriptional Regulatory Region
; FILE REFERENCE: PB1087US4
; CURRENT APPLICATION NUMBER: US/08/481,968A
; CURRENT FILING DATE: 1998-06-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-481-968A-4

Query Match          99.8%; Score 471; DB 3; Length 11288;
Best Local Similarity 100.0%; Pred. No. 8.4e-133;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AGCCACCAACCCAGTGAGCCCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCTCTGTG 60
Db      10294 AGCCACCAACCCAGTGAGCCCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCTCTGTG 10353

Qy      61  GGCATCATCCACCTTCCAGAGCCCTGAGAGCATGGGAGACCCCGGGACCCCTGCTGGG 120
Db      10354 GGCATCATCCACCTTCCAGAGCCCTGAGAGCATGGGAGACCCCGGGACCCCTGCTGGG 10413

Qy      121 TTTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGAACACAG 180
Db      10414 TTTCTCTGTCAAAAGGAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGAACACAG 10473

Qy      181 CAGAGGTGACACTGGGGAAGACAGATTGTCTCCAGGGGATGGGGGTTCATCCACCTT 240
Db      10474 CAGAGGTGACACTGGGGAAGACAGATTGTCTCCAGGGGATGGGGGTTCATCCACCTT 10533

Qy      241 GCCGAAAAGATTGTCTGAGGAACTCAAAAATAGAGGGAAAAAAGAGAGGACAAAGA 300
Db      10534 GCCGAAAAGATTGTCTGAGGAACTCAAAAATAGAGGGAAAAAAGAGAGGAGCAAGA 10593

Qy      301 GGCAGAAATGAGGGGGGGGACAGAGACACTGAATAAAGACCACACCCATGACCCA 360
Db      10594 GGCAGAAATGAGGGGGGGGACAGAGACACTGAATAAAGACCACACCCATGACCCA 10653

Qy      361 CGTGATGCTGAGAAGTACTCTCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db      10654 CGTGATGCTGAGAAGTACTCTCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGACA 10713

Qy      421 GCAGACCAGACAGTCACAGCAGCCTTTGCAAAAAGCTTCTTGGAACTCAAGC 471
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTTGCAAAAAGCTTCTTGGAACTCAAGC 10764

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RESULT 6
 US-08-154-712B-4
 ; Sequence 4, Application US/08154712B
 ; Patent No. 6337209
 ; GENERAL INFORMATION:
 ; APPLICANT: Huber, Brian
 ; APPLICANT: Richards, Cynthia
 ; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Reg
 ; TITLE OF INVENTION: Sequence
 ; FILE REFERENCE: PB1087US3
 ; CURRENT APPLICATION NUMBER: US/08/154,712B
 ; CURRENT FILING DATE: 1993-11-19
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4 :
 ; LENGTH: 11288
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-08-154-712B-4
 Query Match 99.8%; Score 471; DB 3; Length 11288;
 Best Local Similarity 100.0%; Pred. No. 8.4e-133;

	Matches	471;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	AGCCACCACCACTGAGCCTTTTTTCTAGCCCCCAGAGGCACCTCTGTACACCTTCTCCTGTTG	60							
Dd	10294	AGCCACCACCACTGAGCCTTTTTTCTAGCCCCCAGAGGCACCTCTGTACACCTTCTCCTGTTG	10353							
Qy	61	GGCATCATCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG	120							
Dd	10354	GGCATCATCCACTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG	10413							
Qy	121	TTTCTCTGTGCACAAAGGAAAAATAATCCCCTGTGTGCAGACCCCAAAGGACAGAACACAG	180							
Dd	10414	TTTCTCTGTGCACAAAGGAAAAATAATCCCCTGTGTGCAGACCCCAAAGGACAGAACACAG	10473							
Qy	181	CAGAGGTCAGCACTGGGGAGAGCAGGTTGTCTCCAGGGGATGGGGTGTCATCCACCTT	240							
Dd	10474	CAGAGGTCAGCACTGGGGAGAGCAGGTTGTCTCCAGGGGATGGGGTGTCATCCACCTT	10533							
Qy	241	GCCGAAAAGATTGTCTGAGGAACCTGAAATAGAGGGGAAAAAAGNGGGGACAANAAGA	300							
Dd	10534	GCCGAAAAGATTGTCTGAGGAACCTGAAATAGAGGGGAAAAAAGNGGGGACAANAAGA	10593							
Qy	301	GGCAGAAATCAGAGGGGGAGGGGACAGAGCACCTGTAATAAAGACACACCCATGACCCA	360							
Dd	10594	GGCAGAAATCAGAGGGGGAGGGGACAGAGCACCTGTAATAAAGACACACCCATGACCCA	10653							
Qy	361	CGTGATGCTGAGAAGTAGTACTCTGCTCCCTAGGAAGAGACTCAGGGCAGAGGGAAGGACA	420							
Dd	10654	CGTGATGCTGAGAAGTAGTACTCTGCTCCCTAGGAAGAGACTCAGGGCAGAGGGAAGGACA	10713							
Qy	421	GCAGACCAGACGTCACAGCAGCCTTGACAAAACGTTCTCGAACTCAAGC	471							
Dd	10714	GCAGACCAGACGTCACAGCAGCCTTGACAAAACGTTCTCGAACTCAAGC	10764							
RESULT 7										
US-09-947-925A-4										
; Sequence 4, Application US/09947925A										
; Patent No. 6693690										
; GENERAL INFORMATION:										
; APPLICANT: Huber, Brian										
; APPLICANT: Richards, Cynthia										
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic										
; TITLE OF INVENTION: Antigen Regulatory										
; SEQUENCE ID NO.: 1										
; FILE REFERENCE: PB1087U33										
; CURRENT APPLICATION NUMBER: US/09/947,925A										
; CURRENT FILING DATE: 2001-09-06										
; PRIOR FILING DATE: US/08/154,712										
; NUMBER OF SEQ ID NOS: 36										
; SOFTWARE: Patentin version 3.0										
; SEQ ID NO 4										
; LENGTH: 11288										
; TYPE: DNA										
; ORGANISM: Homo sapiens										
US-09-947-925A-4										

Qy	181	CAGAGTTCAGCACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACTT	240
Db	10474	CAGAGTTCAGCACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACTT	10533
Qy	241	GCCGAAAGATTGTCTGAGGAACCTGAAAATAGAAAGGCAAAAAGAGAGGGACAAAGA	300
Db	10534	GCCGAAAGATTGTCTGAGGAACCTGAAAATAGAAAGGCAAAAAGAGAGGGACAAAGA	10593
Qy	301	GGCAGAAATGAGAGGGGAGGGACAGAGGACACCTGAATAAAGACCACCCATGACCCA	360
Db	10594	GGCAGAAATGAGAGGGGAGGGACAGAGGACACCTGAATAAAGACCACCCATGACCCA	10653
Qy	361	CGTGATGCTGAGAAGTACTCTGCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA	420
Db	10654	CGTGATGCTGAGAAGTACTCTGCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA	10713
Qy	421	GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCTGAAACTCAAGC	471
Db	10714	GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCTGAAACTCAAGC	10764
RESULT 8			
US-09-474-699-10			
; Sequence 10, Application US/09474699			
; Patent No. 6495130			
; GENERAL INFORMATION:			
; APPLICANT: Henderson, Daniel R.			
; APPLICANT: Yu, De Chao			
; TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENO VIRAL VECTORS			
; TITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE THEREOF			
; FILE REFERENCE: 348022001300			
; CURRENT APPLICATION NUMBER: US/09/474,699			
; CURRENT FILING DATE: 1999-12-29			
; PRIOR APPLICATION NUMBER: 60/114,262			
; PRIOR FILING DATE: 1998-12-30			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 10			
; LENGTH: 15056			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-09-474-699-10			

Db 14422 CGTGTGCTGAGAGTACTCTGCTCCCTAGGAAGAGACTCAGGGCAGAGGAGGACA 14481
QY 421 GCACACAGACAGTCACAGAGCCTTCACAAACGTTCTGGAACTCAAGC 471
Db 14482 GCAGACCAGACAGTCACAGAGCCTTCGACAAAACGTTCTGGAACTCAAGC 14532
RESULT 9
US-09-814-351-14
; Sequence 14, Application US/09814351
; Patent No. 6692736
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 15056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CEA TRE
US-09-814-351-14

Query Match 99.8%; Score 471; DB 4; Length 15056;
Best Local Similarity 100.0%; Pred. No. 9.6e-133;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCTCTGTTG 60
Db 14062 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCTCTGTTG 14121
QY 61 GGCATCATCCACCTTCCAGAGCCTTGGAGAGCATGGGAGACCCCGGACCTCTGTGGG 120
Db 14122 GGCATCATCCACCTTCCAGAGCCTTGGAGAGCATGGGAGACCCCGGACCTCTGTGGG 14181
QY 121 TTTCTCTGTACAAAGAAATATATCCCTGCTGTGTGACAGACCCCAAGGACAGACACAG 180
Db 14182 TTTCTCTGTACAAAGAAATATATCCCTGCTGTGTGACAGACCCCAAGGACAGACACAG 14241
QY 181 CAGAGGTGACACTGGGGAAGACAGAGTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 14242 CAGAGGTGACACTGGGGAAGACAGAGTGTCTCCAGGGGATGGGGTCCATCCACCTT 14301
QY 241 GCCGAAAAGATTGTCTGAGAACTGAAATAGAGGAAAAAGAGGAGGGAACAAAGA 300
Db 14302 GCCGAAAAGATTGTCTGAGAACTGAAATAGAGGAAAAAGAGGAGGGAACAAAGA 14361
QY 301 GGCAGAAATAGAGGGAGGGGACAGAGGACACTGTAATTAAGACCCACCCATGACCCA 360
Db 14362 GGCAGAAATAGAGGGAGGGGACAGAGGACACTGTAATTAAGACCCACCCATGACCCA 14421
QY 361 CGTGATCTCAGAGTACTCTGCTCCCTAGGAAGACTCAGGGCAGAGGGAGGAGGACA 420
Db 14422 CGTGATCTCAGAGTACTCTGCTCCCTAGGAAGACTCAGGGCAGAGGGAGGAGGACA 14481
QY 421 GCAGACACAGACAGTCACAGAGCCTTGACAAAACGTTCTGGAACTCAAGC 471
Db 14482 GCAGACACAGACAGTCACAGAGCCTTGACAAAACGTTCTGGAACTCAAGC 14532
RESULT 10
US-09-924-103-1
; Sequence 1, Application US/09924103

; Patent No. 6759045
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: IMMUNOTHERAPY FOR CHRONIC MYELOCYTIC LEUKEMIA
; FILE REFERENCE: 018733-1055
; CURRENT APPLICATION NUMBER: US/09/924,103
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-924-103-1
Query Match 33.2%; Score 156.6; DB 4; Length 2073;
Best Local Similarity 76.0%; Pred. No. 1.2e-37;
Matches 247; Conservative 0; Mismatches 69; Indels 9; Gaps 4;
QY 156 TGACAGACCCCAAGGACAGACACAGAGGTCAGACCTGGGGAGACAGAGTTGTCTCTCC 215
Db 220 TGACAGACCCCAAGGACAGACACAGAGGTCAGACCTGGGGAGAGCGGGTCTCTCTGT 279
QY 216 CAGGGGATGGGGTCCATCCACCTT---GCCGAAAAAGATTGTCTGAGAACTGA---A 268
Db 280 TATGGAACAGGGGTCCAAACAGCTTCTTCTCAGAGCATCTTCTGGGACACTGAATATA 339
QY 269 AATAGAAAGGAAAAAGAGAGGGGACAAAAGAGGCGAGAAATAGAGGGAGGAGGACAGAG 328
Db 340 AACAGAAAGGAAAGAGGAGGGGACAAAAGAGACAGAAATAGAGGGAGGAGGATAGAG 399
QY 329 GACACCTGATTAAGACACACCCATGACCCAGCTGATCTGAGAGTACTCT-CCCT 387
Db 400 GATTCCTGAACAGAGACCCGACCCATGACCCAGCTGACCTTGGGAAATGCTTCTATCCCT 459
QY 388 AGAAGAGACTCAGGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 447
Db 460 GAGAGGAGGCTCAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 519
QY 448 A-CAAACTTCTGGAACCTCAAGC 471
Db 520 ACCAGAGCATCTCTGGAGCTCAAGC 544
RESULT 11
US-08-646-301A-2
; Sequence 2, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: PB1508USW
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-646-301A-2
Query Match 41.9%; Score 94; DB 3; Length 3774;
Best Local Similarity 69.5%; Pred. No. 1.7e-18;
Matches 185; Conservative 0; Mismatches 50; Indels 31; Gaps 3;
QY 4 CACACCCAGTGAGCCTTTTCTAGCCCCCAGAGGACCTCTGTCTACCTTCTCTGTGGGC 63
Db 1662 CAGTAAACAGTGAGCTCTATCCAGCCCCCAGAGGACCTCTGTCTACCTTCTCTGTGGGC 1721


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QY 64 ATCATCCACCTTCCAGAGCCTGGAGAGCATGGGAGACCCGGGACCCCTGCTGGGTTT 123
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Db 1898 AGGGACAGGGGTGCACAGCCTTGC 1923

RESULT 12
US-08-481-968A-5
; Sequence 5, Application US/08481968A
; Patent No. 6300490
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA)
; TITLE OF INVENTION: Transcriptional Regulatory Region
; FILE REFERENCE: PBI087US4
; CURRENT APPLICATION NUMBER: US/08/481,968A
; CURRENT FILING DATE: 1998-06-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 3774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-481-968A-5

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Best Local Similarity 69.5%; Pred. No. 1.7e-18;
Matches 185; Conservative 0; Mismatches 50; Indels 31; Gaps 3;

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RESULT 14
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; Sequence 5, Application US/09947925A
; Patent No. 6699690
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
; TITLE OF INVENTION: Antigen Regulatory
; TITLE OF INVENTION: Sequence
; FILE REFERENCE: PBI087US3
; CURRENT APPLICATION NUMBER: US/09/947,925A
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US/08/154,712
; PRIOR FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 3774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-947-925A-5

Query Match 19.9%; Score 94; DB 4; Length 3774;
Best Local Similarity 69.5%; Pred. No. 1.7e-18;
Matches 185; Conservative 0; Mismatches 50; Indels 31; Gaps 3;

QY 4 CACACCCAGTAGGCTTTTCTAGCCCCCAGAGCCACCTCTGTACACCTTCTCTGTGGGC 63
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; Sequence 5, Application US/08154712B
; Patent No. 6337209
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Regu
; TITLE OF INVENTION: Sequence
; FILE REFERENCE: PBI087US3
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; CURRENT APPLICATION NUMBER: US/08/154,712B
; CURRENT FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 3774
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US-08-154-712B-5

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Best Local Similarity 69.5%; Pred. No. 1.7e-18;
Matches 185; Conservative 0; Mismatches 50; Indels 31; Gaps 3;

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RESULT 14
US-09-947-925A-5
; Sequence 5, Application US/09947925A
; Patent No. 6699690
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
; TITLE OF INVENTION: Antigen Regulatory
; TITLE OF INVENTION: Sequence
; FILE REFERENCE: PBI087US3
; CURRENT APPLICATION NUMBER: US/09/947,925A
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US/08/154,712
; PRIOR FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
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; ORGANISM: Homo sapiens
US-09-947-925A-5

Query Match 19.9%; Score 94; DB 4; Length 3774;
Best Local Similarity 69.5%; Pred. No. 1.7e-18;
Matches 185; Conservative 0; Mismatches 50; Indels 31; Gaps 3;

QY 4 CACACCCAGTAGGCTTTTCTAGCCCCCAGAGCCACCTCTGTACACCTTCTCTGTGGGC 63
Db 1662 CAGTAAACAGTAGGCTCTCTATCCAGCCCCCAGAGCCACCTCTGTACACCTTCTCTGTGGGC 1721
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
5744.772 Million cell updates/sec

Title: US-10-045-116-1

Perfect score: 472

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Gapop 10.0 , Gapext 1.0

Searched: 4085731 seqs, 2756760397 residues

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Database : Published Applications NA:*

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- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	472	100.0	472	10	US-09-151-376-54
3	472	100.0	472	14	US-10-045-116-1
4	472	100.0	472	15	US-10-139-089-7
5	472	100.0	472	15	US-10-139-089-54
6	472	100.0	472	18	US-10-822-873-7
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10	471	99.8	15056	9	US-09-392-822-4
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13	471	99.8	15056	14	US-10-045-116-25	Sequence 25, Appl
14	471	99.8	15056	15	US-10-226-820-10	Sequence 10, Appl
15	432.4	91.6	3281	15	US-10-090-238-1	Sequence 1, Appl
16	350.4	74.2	425	14	US-10-212-667-2	Sequence 2, Appl
17	156.6	33.2	2073	9	US-09-924-103-1	Sequence 1, Appl
18	120.8	25.6	1855	13	US-10-027-632-97812	Sequence 97812, A
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20	99.2	21.0	608	13	US-10-027-632-8715	Sequence 8715, Ap
21	99.2	21.0	608	15	US-10-027-632-8715	Sequence 8715, Ap
22	94	19.9	3774	9	US-09-947-925A-5	Sequence 5, Appl
23	75	15.9	2974	9	US-09-954-456-56	Sequence 56, Appl
24	75	15.9	2974	9	US-09-880-107-2317	Sequence 2317, Ap
25	75	15.9	2974	15	US-10-157-031-340	Sequence 340, App
26	75	15.9	2974	15	US-10-207-655-86	Sequence 86, Appl
27	75	15.9	2974	15	US-10-117-937-593	Sequence 593, App
28	75	15.9	2974	15	US-10-295-027-331	Sequence 331, App
29	75	15.9	2974	16	US-10-240-425-1314	Sequence 1314, Ap
30	75	15.9	2974	17	US-10-734-564-5	Sequence 5, Appl
31	75	15.9	2974	17	US-10-657-022-89	Sequence 89, Appl
32	75	15.9	2975	14	US-10-090-326-1	Sequence 1, Appl
33	69.4	14.7	653	11	US-09-969-034-4281	Sequence 4281, Ap
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35	60.6	12.8	474	9	US-09-864-761-6512	Sequence 6512, Ap
36	59	12.5	1298	9	US-09-925-301-290	Sequence 290, App
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38	57.6	12.2	387	9	US-09-854-133-177	Sequence 177, App
39	57.6	12.2	387	15	US-10-144-649A-177	Sequence 177, App
40	57.2	12.1	460	9	US-09-922-217-169	Sequence 169, App
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42	57.2	12.1	460	13	US-10-025-380-169	Sequence 169, App
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C 45	55.4	11.7	294	9	US-09-920-300A-311	Sequence 311, App

ALIGNMENTS

RESULT 1
US-09-151-376-7
; Sequence 7, Application US/09151376
; Publication NO. US20030044383A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D. R.
; APPLICANT: Schuur, E. R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 34802000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-151-376-7

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Db	61	GGCATCATCCACCTTCCAGAGCCCTTGAGAGCATGGGAGACCCGGGACCTCTGTTGG	120	

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RESULT 2
US-09-151-376-54
; Sequence 54, Application US/09151376
; Publication No. US20030044383A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
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; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-151-376-54

Query Match 100.0%; Score 472; DB 10; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-045-116-1
; Sequence 1, Application US/10045116
; Publication No. US20030026792A1
; GENERAL INFORMATION:
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,116
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-045-116-1

Query Match 100.0%; Score 472; DB 14; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-873-7

Query Match 100.0%; Score 472; DB 18; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
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QY 361 CGTATGCTGAGAAGTACTCTCGCCCTAGGAAAGACTCAGGGCAGAGGGAGGAGGAGGAC 420
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QY 421 GCAGACCAGACAGTCAAGAGCCCTTGACAAAACGTTCTCGAACTCAAGCA 472
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RESULT 7

US-10-822-873-54
; Sequence 54, Application US/10822873
; Publication No. US20040241857A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-822-873-54

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Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 TTTCTCTGTCAAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGACAGACACAG 180
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QY 241 GCCGAAAAGATTGTTCTGAGGAACTGAAATAGAGGGAAAAAGAGGGGACAAAAGA 300
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DB 301 GGCAGAAATGAGAGGGAGGGGACAGAGGACACCTGAAATAAAGACACACCCATGACCCA 360
QY 361 CGTGATGCTGAGAACTCTCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
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QY 421 GCAGACACAGACAGTACAGAGGAGCTTGACAAAAAGTTCTGGAACTCAAGCA 472
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RESULT 8
US-09-947-925A-4
; Sequence 4, Application US/09947925A
; Patent No. US20020055482A1
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
; TITLE OF INVENTION: Antigen Regulatory
; TITLE OF INVENTION: Sequence
; FILE REFERENCE: F01087053
; CURRENT APPLICATION NUMBER: US/09/947,925A
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US/08/154,712
; PRIOR FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-947-925A-4

Query Match 99.8%; Score 471; DB 9; Length 11288;
Best Local Similarity 100.0%; Pred. No. 1.4e-135;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACACCCAGTGAAGCTTTTCTAGCCCCCAGAGCCACCTCTGTCACTTCTCTGTTG 60
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QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTCTGCTGGG 120
DB 10354 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTCTGCTGGG 10413

QY 121 TTTCTCTGTCAAAAGGAAATTAATCCCTGTGTGACAGACCCCAAGGACAGAACACAG 180
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QY 181 CAGAGTTCAGACTGGGGAGACAGGTTGTCTCCAGGGGATGGGGGTCCATCCACCTT 240
DB 10474 CAGAGTTCAGACTGGGGAGACAGGTTGTCTCCAGGGGATGGGGGTCCATCCACCTT 10533

QY 241 GCGGAAAAGATTGTTCTGAGGAACTGAAATAGAGGGGAAAAAGAGGGGACAAAAGA 300
DB 10534 GCGGAAAAGATTGTTCTGAGGAACTGAAATAGAGGGGAAAAAGAGGGGACAAAAGA 10593

QY 301 GCGAGAAATGAGAGGGGAGGACAGAGGACACCTGAAATAAAGACACACCCATGACCCA 360
DB 10594 GCGAGAAATGAGAGGGGAGGACAGAGGACACCTGAAATAAAGACACACCCATGACCCA 10653

QY 361 CGTGATGCTGAGAACTCTCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
DB 10654 CGTGATGCTGAGAACTCTCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 10713

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US-09-392-822-4
; Sequence 4, Application US/09392822
; Patent No. US20010053352A1

QY 421 GCAGACACAGACAGTACAGAGCCCTTGACAAAAAGTTCTGGAACTCAAGC 471
DB 10714 GCAGACACAGACAGTACAGAGCCCTTGACAAAAAGTTCTGGAACTCAAGC 10764

RESULT 9
US-09-822-634-1
; Sequence 1, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10804)...(10935)
US-09-822-634-1

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Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTCTGCTGGG 120
DB 10354 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCTCTGCTGGG 10413

QY 121 TTTCTCTGTCAAAAGGAAATTAATCCCTGTGTGACAGACCCCAAGGACAGAACACAG 180
DB 10414 TTTCTCTGTCAAAAGGAAATTAATCCCTGTGTGACAGACCCCAAGGACAGAACACAG 10473

QY 181 CAGAGTTCAGACTGGGGAGACAGGTTGTCTCCAGGGGATGGGGGTCCATCCACCTT 240
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QY 241 GCGGAAAAGATTGTTCTGAGGAACTGAAATAGAGGGGAAAAAGAGGGGACAAAAGA 300
DB 10534 GCGGAAAAGATTGTTCTGAGGAACTGAAATAGAGGGGAAAAAGAGGGGACAAAAGA 10593

QY 301 GCGAGAAATGAGAGGGGAGGACAGAGGACACCTGAAATAAAGACACACCCATGACCCA 360
DB 10594 GCGAGAAATGAGAGGGGAGGACAGAGGACACCTGAAATAAAGACACACCCATGACCCA 10653

QY 361 CGTGATGCTGAGAACTCTCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
DB 10654 CGTGATGCTGAGAACTCTCTCCCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 10713

QY 421 GCAGACACAGACAGTCAAGACCCCTTGACAAAAAGTTCTGGAACTCAAGC 471
DB 10714 GCAGACACAGACAGTCAAGACCCCTTGACAAAAAGTTCTGGAACTCAAGC 10764


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Db      14122 GGCATCATCCACCTTCCAGAGCCTTGAGAGCCTTGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 14181
QY     121  TTTCTCTGTACAAAGGAAATAATCCCTTGGTGTGACAGACCCCAAGGACACAGACACAG 180
Db     14182 TTTCTCTGTACAAAGGAAATAATCCCTTGGTGTGACAGACCCCAAGGACACAGACACAG 14241
QY     181  CAGAGGTGACGACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
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QY     241  GCCGAAAGATTTGTCTGAGGAACCTGAAATAAGAGGGGAAAGAGAGGGGACAAAGA 300
Db     14302 GCCGAAAGATTTGTCTGAGGAACCTGAAATAAGAGGGGAAAGAGAGGGGACAAAGA 14361
QY     301  GGCAGAAATGAGAGGGGAGGACAGAGGACACCTGAATAAAGACACACCCATGACCCA 360
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QY     361  CCGTATGCTGAGAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db     14422 CCGTATGCTGAGAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGGACA 14481
QY     421  GCAGACCACAGACGTACAGCAGCCTTGACAAAACGTTCTGGAACCTCAAGC 471
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; Sequence 1, Application US/10090238
; Publication No. US20030176377A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Rong Xiang
; APPLICANT: Ralph A. Reisfeld
; TITLE OF INVENTION: DNA VACCINES ENCODING CEA AND A CD40
; TITLE OF INVENTION: LIGAND AND METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-830.0
; CURRENT APPLICATION NUMBER: US/10/090,238
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: human
US-10-090-238-1
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Best Local Similarity 98.9%; Pred. No. 9.8e-124;
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QY     61  GGCATCATCCACCTTCCAGAGCCTTGAGAGCCTTGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 120
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QY     121  TTTCTCTGTACAAAGGAAATAATCCCTTGGTGTGACAGACCCCAAGGACACAGACACAG 180
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QY     300 AGGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAAATAAGACCACACCCATGACCC 359
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QY     360 ACGTGATGCTGAGAAAGTACTCTGCCCCTAGGAAGAGACTCAGGGGACAGAGGGAGGAGGAC 419
Db     1618 ACGTGATGCTGAGAAAGTACTCTGCCCCTAGGAAGAGACTCAGGGGACAGAGGGAGGAGGAC 1677
QY     420 AGCAGACCACAGACAGTCAAGCAGCAGCCTTGACAAAACGTTCTTGGAACTCAAGC 471
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Db 421 GCAGACAGACAGTCAAGCAGCCTTGACAAAACGTTCTGGAACCTCAAGCA 472

RESULT 2
US-09-033-555A-1
; Sequence 1, Application US/09033555A
; GENERAL INFORMATION:
; APPLICANT: Lampareki, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-033-555A-1

Query Match 100.0%; Score 472; DB 15; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-114;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCTGTTG 60
Db 1 AGCCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCTGTTG 60

QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCTGCTGGG 120
Db 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCTGCTGGG 120

QY 121 TTTCTCTGTCAAAAGGAAAAATAATCCCTCGTGTGACAGACCCCAAGGACACAG 180
Db 121 TTTCTCTGTCAAAAGGAAAAATAATCCCTCGTGTGACAGACCCCAAGGACACAG 180

QY 181 CAGAGTTCAGCTGGGAGAGCAGGTTCTCTCCAGGGGATGGGGTCCATCCACTT 240
Db 181 CAGAGTTCAGCTGGGAGAGCAGGTTCTCTCCAGGGGATGGGGTCCATCCACTT 240

QY 241 GCCGAAAGATTGTCTGAGGAATGAAATAGAGGAAAAAGAGGAGGACAAAGA 300
Db 241 GCCGAAAGATTGTCTGAGGAATGAAATAGAGGAAAAAGAGGAGGACAAAGA 300

QY 301 GGCAGAAATGAGAGGGGAGGACAGAGCACCTTGAATAAAGCACCAATGACCCA 360
Db 301 GGCAGAAATGAGAGGGGAGGACAGAGCACCTTGAATAAAGCACCAATGACCCA 360

Db 301 GCGAGAAATGAGAGGGGAGGACAGAGCACCTTGAATAAAGACACCAATGACCCA 360

QY 361 CGTGATGCTGAGAGTACTCTCCCTAGGAAGAGACTCAGGCGAGAGGAGGAGCA 420
Db 361 CGTGATGCTGAGAGTACTCTCCCTAGGAAGAGACTCAGGCGAGAGGAGGAGCA 420

QY 421 GCGAGACCCAGACAGTCAAGCAGCCTTGACAAAACGTTCTGGAACCTCAAGCA 472
Db 421 GCGAGACCCAGACAGTCAAGCAGCCTTGACAAAACGTTCTGGAACCTCAAGCA 472

RESULT 3
US-10-045-116-1
; Sequence 1, Application US/10045116
; GENERAL INFORMATION:
; APPLICANT: Lampareki, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,116
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-045-116-1

Query Match 100.0%; Score 472; DB 45; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-114;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCTGTTG 60
Db 1 AGCCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTACCTTCTGTTG 60

QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCTGCTGGG 120
Db 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGACCTGCTGGG 120

QY 121 TTTCTCTGTCAAAAGGAAAAATAATCCCTCGTGTGACAGACCCCAAGGACACAG 180
Db 121 TTTCTCTGTCAAAAGGAAAAATAATCCCTCGTGTGACAGACCCCAAGGACACAG 180

181	Qy	CAGAGGTCAGCACTGGGGAAGACAGTTTGTCTCCACGGGATGGGGTCCATCCACCTT	240
181	Db	CAGAGGTCAGCACTGGGGAAGACAGTTTGTCTCCACGGGATGGGGTCCATCCACCTT	240
241	Qy	GCCGAAACAGATTTGTCTGAGGAACCTGAAAATAGAAAGGGAAGAGAGGGGCAAAAGA	300
241	Db	GCCGAAACAGATTTGTCTGAGGAACCTGAAAATAGAAAGGGAAGAGAGGGGCAAAAGA	300
301	Qy	GGCAGAAATAGAGGGGAGGGGACAGAGGACACCTGAAATAAGACCAACCCATGACCCA	360
301	Db	GGCAGAAATAGAGGGGAGGGGACAGAGGACACCTGAAATAAGACCAACCCATGACCCA	360
361	Qy	CTGTATGCTCGAAGTACTCTTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGAGCA	420
361	Db	CTGTATGCTCGAAGTACTCTTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAGAGCA	420
421	Qy	GCAGCCAGACAGTCACAGACGCTTGACAAAACGTTCTCTGGAACTCAAGCA	472
421	Db	GCAGCCAGACAGTCACAGACGCTTGACAAAACGTTCTCTGGAACTCAAGCA	472

RESULT 4

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US-10-139-089-7
; Sequence 7, Application US/10139089
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/10/139,089
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; PRIOR APPLICATION NUMBER: 09/509,591
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/033,428
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,597
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,555
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,763
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,333
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,762
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-139-089-7

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121  TTTCTCTGT CACAAAGGAAAATATCCCTCGGTGT CAGACCCAAAGGACAGAACAG 180
181  CAGAGGT CAGCACTGGGGAAAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
181  CAGAGGT CAGCACTGGGGAAAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
241  GCCGAAAGAATTTGTTCTGTAGGAACTGAAAATAGAAAGGAAAGAGAGAGGACAAAAGA 300
241  GCCGAAAGAATTTGTTCTGTAGGAACTGAAAATAGAAAGGAAAGAGAGAGGACAAAAGA 300
301  GGCAGAATCAGAGGGGGAGGGGACAGAGGACACCTGAAATAAGAGACCACACCCTGACCCA 360
301  GGCAGAATCAGAGGGGGAGGGGACAGAGGACACCTGAAATAAGAGACCACACCCTGACCCA 360
361  CGTGATGCTCAGAAGTACTCCTGCGCTTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
361  CGTGATGCTCAGAAGTACTCCTGCGCTTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
421  GCAGACCAGACGTCACAGCAGCGCTTCACAAAGCTTCCCTGGAACCTCAAGCA 472
421  GCAGACCAGACGTCACAGCAGCGCTTGCACAAACGTTTCCTGGAACTCAAGCA 472

RESULT 5
US-10-139-089-54
; Sequence 54, Application US/10139089
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS

```

RESIST. 5

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US-10-139-089-54
; Sequence 54, Application US/10139089
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 34802200221
; CURRENT APPLICATION NUMBER: US/10/139,089
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; PRIOR APPLICATION NUMBER: 03/509,591
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/033,428
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,597
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,555
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,763
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,333
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,762
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-139-089-54

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Db 61 GGCAATCATCCACCTTCCAGAGCCCTGGAGAGCTGGGGAGACCCGGGACCTGCTGGG 120
Qy 121 TTCTCTGTGCACAAAGGAAAAAATATCCCTCGTGTGACAGACCCAGGAGACACACAG 180
Db 121 TTCTCTGTGCACAAAGGAAAAAATATCCCTCGTGTGACAGACCCAGGAGACACACAG 180
Qy 181 CAGAGTTCAGCACTGGGGAGAGCAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 181 CAGAGTTCAGCACTGGGGAGAGCAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Qy 241 GCCGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAAGAGGAGGACAAAAGA 300
Db 241 GCCGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAAGAGGAGGACAAAAGA 300
Qy 301 GCGAGAAATGAGAGGGGGGAGGAGGACAGGACACCTGAATAAGAGCCACACCCATGACCCA 360
Db 301 GCGAGAAATGAGAGGGGGGAGGAGGACAGGACACCTGAATAAGAGCCACACCCATGACCCA 360
Qy 361 CGTGATCTGAGAAGTACTCTGCGCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db 361 CGTGATCTGAGAAGTACTCTGCGCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Qy 421 CGAGACACAGACAGTCAAGAGCCTTTCGCAAAACGTTCTGGAACCTCAAGCA 472
Db 421 CGAGACACAGACAGTCAAGAGCCTTTCGCAAAACGTTCTGGAACCTCAAGCA 472

RESULT 6

US-10-822-873-7
; Sequence 7, Application US/10822873
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR FILING DATE: 1998-09-10
; PRIOR FILING DATE: 1998-09-10
; PRIOR FILING DATE: 1996-06-26
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-873-7

Query Match 100.0%; Score 472; DB 62; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-114;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCACACCCAGTGAAGCCTTTTCTAGCCCCCAGAGCACCCTCTGTCACTTCTCTGTTG 60
Db 1 AGCCACACCCAGTGAAGCCTTTTCTAGCCCCCAGAGCACCCTCTGTCACTTCTCTGTTG 60
Qy 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 120
Db 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 120
Qy 121 TTCTCTGTGCACAAAGGAAAAAATATCCCTCGTGTGACAGACCCAGGAGGACAAACAG 180
Db 121 TTCTCTGTGCACAAAGGAAAAAATATCCCTCGTGTGACAGACCCAGGAGGACAAACAG 180
Qy 181 CAGAGTTCAGCACTGGGGAGAGCAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 181 CAGAGTTCAGCACTGGGGAGAGCAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240

Qy 241 GCCGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAAGAGGAGGACAAAAGA 300
Db 241 GCCGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAAGAGGAGGACAAAAGA 300
Qy 301 GCGAGAAATGAGAGGGGGGAGGAGGACAGGACACCTGAATAAGAGCCACACCCATGACCCA 360
Db 301 GCGAGAAATGAGAGGGGGGAGGAGGACAGGACACCTGAATAAGAGCCACACCCATGACCCA 360
Qy 361 CGTGATCTGAGAAGTACTCTGCGCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Db 361 CGTGATCTGAGAAGTACTCTGCGCTAGGAGAGACTCAGGGCAGAGGGAGGAGGACA 420
Qy 421 CGAGACACAGACAGTCAAGAGCCTTTCGCAAAACGTTCTGGAACCTCAAGCA 472
Db 421 CGAGACACAGACAGTCAAGAGCCTTTCGCAAAACGTTCTGGAACCTCAAGCA 472

RESULT 7

US-10-822-873-54
; Sequence 54, Application US/10822873
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-822-873-54

Query Match 100.0%; Score 472; DB 62; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-114;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCACACCCAGTGAAGCCTTTTCTAGCCCCCAGAGCACCCTCTGTCACTTCTCTGTTG 60
Db 1 AGCCACACCCAGTGAAGCCTTTTCTAGCCCCCAGAGCACCCTCTGTCACTTCTCTGTTG 60
Qy 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 120
Db 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 120
Qy 121 TTCTCTGTGCACAAAGGAAAAAATATCCCTCGTGTGACAGACCCAGGAGGACAAACAG 180
Db 121 TTCTCTGTGCACAAAGGAAAAAATATCCCTCGTGTGACAGACCCAGGAGGACAAACAG 180
Qy 181 CAGAGTTCAGCACTGGGGAGAGCAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 181 CAGAGTTCAGCACTGGGGAGAGCAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Qy 241 GCCGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAAGAGGAGGACAAAAGA 300
Db 241 GCCGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAAGAGGAGGACAAAAGA 300
Qy 301 GCGAGAAATGAGAGGGGGGAGGAGGACAGGACACCTGAATAAGAGCCACACCCATGACCCA 360
Db 301 GCGAGAAATGAGAGGGGGGAGGAGGACAGGACACCTGAATAAGAGCCACACCCATGACCCA 360

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QY 361 CQTGATGCTGAGAAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
Db 361 CQTGATGCTGAGAAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
QY 421 GCAGACCCAGACAGTACAGCAGCCCTTGACAAACCTTCTCTGGAACCTCAAGCA 472
Db 421 GCAGACCCAGACAGTACAGCAGCCCTTGACAAACCTTCTCTGGAACCTCAAGCA 472

RESULT 8
US-10-486-319A-11
; Sequence 11, Application US/10486319A
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/486,319A
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 527
; SEQ ID NO 11
; LENGTH: 3500
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-486-319A-11

Query Match 99.8%; Score 471; DB 54; Length 3500;
Best Local Similarity 100.0%; Pred. No. 9.9e-114;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTGCACCTTCTCTGTTG 60
Db 2506 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTGCACCTTCTCTGTTG 2565
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGAGCCCTGCTGGG 120
Db 2566 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGAGCCCTGCTGGG 2625
QY 121 TTTCTCTGTCAAAAAGGAAATATCCCTTGGTGTGACAGACCCCAAGGACAGACACAG 180
Db 2626 TTTCTCTGTCAAAAAGGAAATATCCCTTGGTGTGACAGACCCCAAGGACAGACACAG 2685
QY 181 CAGAGGTCAGCAGCTGGGGAAGACAGAGTTGTCTCCAGGGATGGGGTCCATCCACCTT 240
Db 2686 CAGAGGTCAGCAGCTGGGGAAGACAGAGTTGTCTCCAGGGATGGGGTCCATCCACCTT 2745
QY 241 CCCGAAAAGATTTGTCTGAGGAACCTGAAATATAGAAAGGAAAAAAGAGAGGACAAAGA 300
Db 2746 CCCGAAAAGATTTGTCTGAGGAACCTGAAATATAGAAAGGAAAAAAGAGAGGACAAAGA 2805
QY 301 GGCAGAAATGAGAGGGGGAGGAGACAGAGGACACCTGAATTAAGACCACCCATGACCCA 360
Db 2806 GGCAGAAATGAGAGGGGGAGGAGACAGAGGACACCTGAATTAAGACCACCCATGACCCA 2865
QY 361 CGTGATGCTGAGAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
Db 2866 CGTGATGCTGAGAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 2925
QY 421 GCAGACCCAGACAGTACAGCAGCCCTTGACAAACCTTCTCTGGAACCTCAAGC 471
Db 2926 GCAGACCCAGACAGTACAGCAGCCCTTGACAAACCTTCTCTGGAACCTCAAGC 2976

RESULT 9
US-10-486-319B-11
; Sequence 11, Application US/10486319B
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
; FILE REFERENCE: 82196
; CURRENT APPLICATION NUMBER: US/10/486,319B
; CURRENT FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 527
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; SEQ ID NO 11
; LENGTH: 3500
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-486-319B-11

Query Match 99.8%; Score 471; DB 54; Length 3500;
Best Local Similarity 100.0%; Pred. No. 9.9e-114;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTGCACCTTCTCTGTTG 60
Db 2506 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTGCACCTTCTCTGTTG 2565
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGAGCCCTGCTGGG 120
Db 2566 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCCGGAGCCCTGCTGGG 2625
QY 121 TTTCTCTGTCAAAAAGGAAATATCCCTTGGTGTGACAGACCCCAAGGACAGACACAG 180
Db 2626 TTTCTCTGTCAAAAAGGAAATATCCCTTGGTGTGACAGACCCCAAGGACAGACACAG 2685
QY 181 CAGAGGTCAGCAGCTGGGGAAGACAGAGTTGTCTCCAGGGATGGGGTCCATCCACCTT 240
Db 2686 CAGAGGTCAGCAGCTGGGGAAGACAGAGTTGTCTCCAGGGATGGGGTCCATCCACCTT 2745
QY 241 CCCGAAAAGATTTGTCTGAGGAACCTGAAATATAGAAAGGAAAAAAGAGAGGACAAAGA 300
Db 2746 CCCGAAAAGATTTGTCTGAGGAACCTGAAATATAGAAAGGAAAAAAGAGAGGACAAAGA 2805
QY 301 GGCAGAAATGAGAGGGGGAGGAGACAGAGGACACCTGAATTAAGACCACCCATGACCCA 360
Db 2806 GGCAGAAATGAGAGGGGGAGGAGACAGAGGACACCTGAATTAAGACCACCCATGACCCA 2865
QY 361 CGTGATGCTGAGAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
Db 2866 CGTGATGCTGAGAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 2925
QY 421 GCAGACCCAGACAGTACAGCAGCCCTTGACAAACCTTCTCTGGAACCTCAAGC 471
Db 2926 GCAGACCCAGACAGTACAGCAGCCCTTGACAAACCTTCTCTGGAACCTCAAGC 2976

RESULT 10
PCT-US04-13487-1
; Sequence 1, Application PC/TUS0413487
; GENERAL INFORMATION:
; APPLICANT: DONG, JIAN-YUN
; APPLICANT: RUBINCHIK, SEMYON
; APPLICANT: WORARATANADHARM, JAN
; TITLE OF INVENTION: AN AUTOLOGOUS UPREGULATION MECHANISM ALLOWING OPTIMIZED
; TITLE OF INVENTION: CELL TYPE-SPECIFIC AND REGULATED GENE EXPRESSION CELLS
; FILE REFERENCE: MESC:014WO
; CURRENT APPLICATION NUMBER: PCT/US04/13487
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/467,171
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10804)..(10938)
PCT-US04-13487-1

Query Match 99.8%; Score 471; DB 2; Length 11288;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTGCACCTTCTCTGTTG 60
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Db 10294 AGCCACCCAGTGGAGCTTTTCTAGCCCCAGAGCCACCTGTGTCACTTCTCTGTG 10353
Qy 61 GGCATCATCCACCTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGTGGG 120
Db 10354 GGCATCATCCACCTTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGTGGG 10413
Qy 121 TTTCTCTGTACAAAGAAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
Db 10414 TTTCTCTGTACAAAGAAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 10473
Qy 181 CAGAGTCTAGCCTGGGGAAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 10474 CAGAGTCTAGCCTGGGGAAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 10533
Qy 241 GCGGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAGAGGAGGACAAAAGA 300
Db 10534 GCGGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAGAGGAGGACAAAAGA 10593
Qy 301 GCGGAAAATGAGAGGGGAGGAGACAGGACACCTGAAATAAGACCCACACCCATGACCCA 360
Db 10594 GCGGAAAATGAGAGGGGAGGAGACAGGACACCTGAAATAAGACCCACACCCATGACCCA 10653
Qy 361 CGTGATGCTGAGAAGTACTCTGCCCTAGGAAAGACACTCAGGGCAGAGGGAGGAAAGGACA 420
Db 10654 CGTGATGCTGAGAAGTACTCTGCCCTAGGAAAGACACTCAGGGCAGAGGGAGGAAAGGACA 10713
Qy 421 GCAGACACAGTCTACAGAGCCTTGACAAAACGTTCTGGAACCTCAAGC 471
Db 10714 GCAGACACAGTCTACAGAGCCTTGACAAAACGTTCTGGAACCTCAAGC 10764
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RESULT 11

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US-07-841-961-6
; Sequence 6, Application US/07841961
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia A
; APPLICANT: Krenitsky, Thomas A
; TITLE OF INVENTION: NOVEL ENTITIES FOR CANCER THERAPY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Donald Brown; Dike, Bronstein, Roberts &
; ADDRESS: Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109-4280
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,961
; FILING DATE: 19920226
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Donald
; REGISTRATION NUMBER: 20845
; REFERENCE/DOCKET NUMBER: 40361-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11288 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10804..10866
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 10281..11288
US-07-841-961-6
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Query Match 99.8%; Score 471; DB 4; Length 11288;

Best Local Similarity 100.0%; Pred. No. 1.5e-113; Indels 0; Gaps 0;

Matches 471; Conservative 0; Mismatches 0;

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Qy 1 AGCCACCCAGTGGAGCTTTTCTAGCCCCAGAGCCACCTGTGTCACTTCTCTGTG 60
Db 10294 AGCCACCCAGTGGAGCTTTTCTAGCCCCAGAGCCACCTGTGTCACTTCTCTGTG 10353
Qy 61 GGCATCATCCACCTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGTGGG 120
Db 10354 GGCATCATCCACCTTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGTGGG 10413
Qy 121 TTTCTCTGTACAAAGGAAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 180
Db 10414 TTTCTCTGTACAAAGGAAAATAATCCCTCTGTGTGACAGACCCCAAGGACAGACACAG 10473
Qy 181 CAGAGTCTAGCCTGGGGAAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 10474 CAGAGTCTAGCCTGGGGAAGACAGGTTGTCTCTCCAGGGGATGGGGTCCATCCACCTT 10533
Qy 241 GCGGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAGAGGAGGACAAAAGA 300
Db 10534 GCGGAAAAGATTGTCTGAGGAACCTGAAAATAGAGGGGAAAAGAGGAGGACAAAAGA 10593
Qy 301 GCGGAAAATGAGAGGGGAGGAGACAGGACACCTGAAATAAGACCCACACCCATGACCCA 360
Db 10594 GCGGAAAATGAGAGGGGAGGAGACAGGACACCTGAAATAAGACCCACACCCATGACCCA 10653
Qy 361 CGTGATGCTGAGAAGTACTCTGCCCTAGGAAAGACACTCAGGGCAGAGGGAGGAAAGGACA 420
Db 10654 CGTGATGCTGAGAAGTACTCTGCCCTAGGAAAGACACTCAGGGCAGAGGGAGGAAAGGACA 10713
Qy 421 GCAGACACAGTCTACAGAGCCTTGACAAAACGTTCTGGAACCTCAAGC 471
Db 10714 GCAGACACAGTCTACAGAGCCTTGACAAAACGTTCTGGAACCTCAAGC 10764
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RESULT 12

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US-08-474-420-4
; Sequence 4, Application US/08474420
; GENERAL INFORMATION:
; APPLICANT: HUBER, BRIAN
; APPLICANT: RICHARDS, CYNTHIA A
; APPLICANT: AUSTIN, ELIZABETH A
; TITLE OF INVENTION: NOVEL ENTITIES FOR CANCER THERAPY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ, P.C.
; STREET: SUITE 701 EAST TOWER, 555 13TH ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,420
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,712
; FILING DATE: 19-NOV-1993
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/841,961
;; FILING DATE: 26-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/662,222
;; FILING DATE: 22-FEB-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/574,994
;; FILING DATE: 29-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: UK 8919607.5
;; FILING DATE: 30-AUG-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: NEWLAND, BART
;; REFERENCE/DOCKET NUMBER: 1808-188A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-783-6040
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11288 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
US-08-474-420-4

Query Match 99.8%; Score 471; DB 9; Length 11288;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACCCAGTCAGTGGAGCCCTTTCTAGCCCCAGAGCCACCTCTGTACCTTCTCTGTTG 60
Db 10294 AGCCACCCAGTCAGTGGAGCCCTTTCTAGCCCCAGAGCCACCTCTGTACCTTCTCTGTTG 10353
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 120
Db 10354 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 10413
QY 121 TTTCTCTGTCAAAAGGAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACACAG 180
Db 10414 TTTCTCTGTCAAAAGGAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACACAG 10473
QY 181 CAGAGTCAGCAGTGGGAGAGCAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 10474 CAGAGTCAGCAGTGGGAGAGCAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 10533
QY 241 GCCGAAAAGATTGTCTGAGGAACCTGAAATAGAGGGGAAAGAGGAGGAGCAAAAAGA 300
Db 10534 GCCGAAAAGATTGTCTGAGGAACCTGAAATAGAGGGGAAAGAGGAGGAGCAAAAAGA 10593
QY 301 GGCAGAAATGAGAGGGGGGAGAGAGACACCTTGAATAAGACCAACCCATGACCCA 360
Db 10594 GGCAGAAATGAGAGGGGGGAGAGAGACACCTTGAATAAGACCAACCCATGACCCA 10653
QY 361 CGTGATGCTGAGAAGTACTCTCCCTAGGAAGAGACTCAGGGGAGAGGGAGGAGGACA 420
Db 10654 CGTGATGCTGAGAAGTACTCTCCCTAGGAAGAGACTCAGGGGAGAGGGAGGAGGACA 10713
QY 421 GCAGACCAAGAGTCAAGCAGCCCTTGACAAAACGTTCTGGAATCTCAAGC 471
Db 10714 GCAGACCAAGAGTCAAGCAGCCCTTGACAAAACGTTCTGGAATCTCAAGC 10764

RESULT 13
US-08-547-142-4
; Sequence 4, Application US/08547142
; GENERAL INFORMATION:
; APPLICANT: HUBER, BRIAN
; APPLICANT: RICHARDS, CYNTHIA A

;; APPLICANT: AUSTIN, ELIZABETH A
;; TITLE OF INVENTION: NOVEL ENTITIES FOR CANCER THERAPY
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ, P.C.
;; STREET: SUITE 701 EAST TOWER, 555 13TH ST., N.W.
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/547,142
;; FILING DATE: 24-OCT-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/154,712
;; FILING DATE: 19-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/841,961
;; FILING DATE: 26-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/662,222
;; FILING DATE: 22-FEB-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/574,994
;; FILING DATE: 29-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: UK 8919607.5
;; FILING DATE: 30-AUG-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: NEWLAND, BART
;; REFERENCE/DOCKET NUMBER: 1808-190A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-783-6040
;; TELEFAX: 202-783-6031
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11288 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
US-08-547-142-4

Query Match 99.8%; Score 471; DB 10; Length 11288;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCACCCAGTCAGTGGAGCCCTTTCTAGCCCCAGAGCCACCTCTGTACCTTCTCTGTTG 60
Db 10294 AGCCACCCAGTCAGTGGAGCCCTTTCTAGCCCCAGAGCCACCTCTGTACCTTCTCTGTTG 10353
QY 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 120
Db 10354 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG 10413
QY 121 TTTCTCTGTCAAAAGGAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACACAG 180
Db 10414 TTTCTCTGTCAAAAGGAAATAATCCCTTGTGTGACAGACCCCAAGGACAGACACAG 10473
QY 181 CAGAGTCAGCAGTGGGAGAGCAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 10474 CAGAGTCAGCAGTGGGAGAGCAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 10533
QY 241 GCCGAAAAGATTGTCTGAGGAACCTGAAATAGAGGGGAAAGAGGAGGAGCAAAAAGA 300

Db 10534 GCGGAAAGATTGTCTGAGAACTGAAATAGAGGGAATAAGAGGGAACAAGA 10593
Qy 301 GCGAGAAATGAGAGGGGAGGAGAGAGGACACCTGATTAAGAGACACACCCATGACCA 360
Db 10594 GCGAGAAATGAGAGGGGAGGAGAGGAGACACCTGATTAAGAGACACACCCATGACCA 10653
Qy 361 CGTGATGCTGAGAAGTACTCTGCCCTAGGAAGAGACTCAGGGGAGAGGAGGAGGAGCA 420
Db 10654 CGTGATGCTGAGAAGTACTCTGCCCTAGGAAGAGACTCAGGGGAGAGGAGGAGGAGCA 10713
Qy 421 GCGAGACAGACAGTACAGACAGCCCTTGACAAAACGTTCTGGAACCTCAAGC 471
Db 10714 GCGAGACAGACAGTACAGACAGCCCTTGACAAAACGTTCTGGAACCTCAAGC 10764

RESULT 14
US-09-822-634-1
; Sequence 1, Application US/09822634
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10804)....(10935)
US-09-822-634-1

Query Match 99.8%; Score 471; DB 34; Length 11288;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCACACCCAGTGAGCCCTTTTCTAGCCCCAGAGCCACTCTGTGACCTTCTCTGTTG 60
Db 10294 AGCCACACCCAGTGAGCCCTTTTCTAGCCCCAGAGCCACTCTGTGACCTTCTCTGTTG 10353

Qy 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGAGCCCTGCTGG 120
Db 10354 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGAGCCCTGCTGG 10413

Qy 121 TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGAGACACACAG 180
Db 10414 TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGAGACACACAG 10473

Qy 181 CAGAGGTACAGACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 10474 CAGAGGTACAGACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 10533

Qy 241 GCGGAAAGATTGTCTGAGGAACTGAAATAGAGGGAATAAGAGGAGGAGGAGCAAGA 300
Db 10534 GCGGAAAGATTGTCTGAGGAACTGAAATAGAGGGAATAAGAGGAGGAGGAGGAGCAAGA 10593

Qy 301 GCGAGAAATGAGAGGGGAGGAGGAGGACACCTGATTAAGAGACACACCCATGACCA 360
Db 10594 GCGAGAAATGAGAGGGGAGGAGGAGGAGGACACCTGATTAAGAGACACACCCATGACCA 10653

Qy 361 CGTGATGCTGAGAAGTACTCTGCCCTAGGAAGAGACTCAGGGGAGAGGAGGAGGAGCA 420
Db 10654 CGTGATGCTGAGAAGTACTCTGCCCTAGGAAGAGACTCAGGGGAGAGGAGGAGGAGCA 10713

Qy 421 GCGAGACAGACAGTACAGACAGCCCTTGACAAAACGTTCTGGAACCTCAAGC 471
Db 10714 GCGAGACAGACAGTACAGACAGCCCTTGACAAAACGTTCTGGAACCTCAAGC 10764

RESULT 15
US-09-033-555A-25
; Sequence 25, Application US/09033555A
; GENERAL INFORMATION:
; APPLICANT: Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING CARCINOEMERYONIC ANTIGENS AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15056 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-033-555A-25

Query Match 99.8%; Score 471; DB 15; Length 15056;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCCACACCCAGTGAGCCCTTTTCTAGCCCCAGAGCCACTCTGTGACCTTCTCTGTTG 60
Db 14062 AGCCACACCCAGTGAGCCCTTTTCTAGCCCCAGAGCCACTCTGTGACCTTCTCTGTTG 14121

Qy 61 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGAGCCCTGCTGG 120
Db 14122 GGCATCATCCACCTTCCAGAGCCCTGGAGAGCATGGGAGACCCGGGAGCCCTGCTGG 14181

Qy 121 TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGAGGAGGAGCAAGA 180
Db 14182 TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGAGGAGGAGCAAGA 14241

Qy 181 CAGAGGTACAGACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 240
Db 14242 CAGAGGTACAGACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTT 14301

Qy 241 GCGGAAAGATTGTCTGAGGAACTGAAATAGAGGGAATAAGAGGAGGAGGAGCAAGA 300
Db 14302 GCGGAAAGATTGTCTGAGGAACTGAAATAGAGGGAATAAGAGGAGGAGGAGGAGCAAGA 14361

QY	301	GGCAGAAATGAGAGGGGAGGACAGAGGACACCTGATTAAGACCAACCCATGACCCA	360
Db	14362	GGCAGAAATGAGAGGGGAGGACAGAGGACACCTGATTAAGACCAACCCATGACCCA	14421
QY	361	CCTGATGCTGAGAAAGTACTCTGCCCTAGGAAAGAGACTCAGGGCAGAGGGAGGAGGACA	420
Db	14422	CCTGATGCTGAGAAAGTACTCTGCCCTAGGAAAGAGACTCAGGGCAGAGGGAGGAGGACA	14481
QY	421	GCAGACCAAGACAGTCAAGAGCCTTGACAAAACGTTCTGGAAGTCAAGC	471
Db	14482	GCAGACCAAGACAGTCAAGAGCCTTGACAAAACGTTCTGGAAGTCAAGC	14532

Search completed: December 11, 2004, 09:53:13
Job time : 3799 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 06:59:48 ; Search time 158 Seconds
(without alignments)
4578.586 Million cell updates/sec

Title: US-10-045-116-1

Perfect score: 472

Sequence: 1 AGCCACCACCCAGTGAGCCT.....ACGTTCTGGAAGCA 472

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1633475 seqs, 766331085 residues

Total number of hits satisfying chosen parameters: 3266950

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA New:*
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
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8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	263.2	55.8	15862	6	US-10-737-082-14
2	103.2	21.9	22140	6	US-10-737-082-68
3	75	15.9	2799	6	US-10-912-745A-360
4	75	15.9	2799	8	US-60-625-561-294
5	75	15.9	2799	8	US-60-625-562-301
6	75	15.9	2974	6	US-10-482-029-240
7	75	15.9	2974	8	US-60-625-561-293
8	75	15.9	2974	8	US-60-625-562-300
9	75	15.9	2976	6	US-10-912-745A-361
10	75	15.9	2976	6	US-60-625-561-292
11	75	15.9	2976	8	US-60-625-562-299
12	55.4	11.7	294	6	US-10-961-527-311
13	43.2	9.2	366	6	US-10-948-737-3964
14	43.2	9.2	472	6	US-10-948-737-3813
15	39.4	8.3	54574	6	US-10-990-328-95976
16	38	8.1	239	6	US-10-220-366A-11800
17	37.6	8.0	312644	6	US-10-990-328-96981
18	37.4	7.9	13277	6	US-10-990-328-96790
19	37.4	7.9	98757	6	US-10-990-328-94219
20	37.2	7.9	98532	6	US-10-990-328-95593
21	37	7.8	432	6	US-10-220-366A-12791
22	37	7.8	574	6	US-10-863-332-33
23	36.6	7.8	206746	6	US-10-990-328-97314
24	36.2	7.7	1285	6	US-10-220-366A-6728
25	36.2	7.7	9535	6	US-10-912-745A-371

ALIGNMENTS

RESULT 1

US-10-737-082-14

; Sequence 14, Application US/10737082

; GENERAL INFORMATION:

; APPLICANT: Bayer Healthcare LLC

; APPLICANT: Beard, Chris

; APPLICANT: Burgess, Chris

; APPLICANT: Gannon, Allison

; APPLICANT: Harvey, Jeanne

; APPLICANT: Lechner, John F.

; APPLICANT: Li, Zheng

; TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences

; FILE REFERENCE: 1657/2032

; CURRENT APPLICATION NUMBER: US/10/737,082

; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 10/737,082

; PRIOR FILING DATE: 2003-12-16

; NUMBER OF SEQ ID NOS: 300

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 14

; LENGTH: 15862

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-737-082-14

Query Match 55.8%; Score 263.2; DB 6; Length 15862;

Best Local Similarity 80.1%; Pred. No. 1.3e-63; Mismatches 63; Indels 32; Gaps 5;

Matches 383; Conservative 0;

QY	1	AGCCACCACCCAGTGAGCCTTTTCTAGCCCCCAGAGCCACCTCTGTCTACCTTCTCTGTTG	60
Db	515	AGTCATCCCCAGTGAGCCCTTTCTATCCCCCAGAGCCACCTCTGTCTACCTTCTCTGCTG	574
QY	61	GGCATCATCCCACTTCCCGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG	120
Db	575	GGCATCATCCCACTTCCCGAGAGCATGGGGAGACCCGGGACCCCTGCTGGG	610
QY	121	TTTCTCTGTACAAAGGAAATAATCCCTCGTGTGACAGACCCCAAGGACACAGACACAG	180
Db	611	TTTCTCTGTGTAC-AAGGAAATAATCCCTCGTGTGACAGACCCCAAGGACACAGACACAG	669
QY	181	CAGAGGTGAGCACTGGGGAAGACAGGTTGTCTCCAGGGGATGGGGGTTCATCCACCTT	240
Db	670	CATAGTGTGAGCACTGGGGAAGGTTGTGTCTCTCCAGGGGACAGGGGTTCATCAGCCTT	729
QY	241	GC--CGAAAAGATTGTCTGTGAGGAAGTGAATAAG--AAGGAAAAAAGAGAGGGGAC	294
Db	730	GCTACTCAAGCTTTGTATCGGGAAGTGAATAAGGAAAGGAAAGAGAGGGGAC	789


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; Sequence 301, Application US/60625562
; GENERAL INFORMATION:
; APPLICANT: MCCAFFREY, Ian
; TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001555
; CURRENT APPLICATION NUMBER: US/60/625,562
; CURRENT FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-625-562-301

Query Match      15.9%; Score 75; DB 8; Length 2799;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 397 CTCAGGCGCAGGGAGGAGGACGACGACCAGCAGTCACAGCAGCCCTTGACAAAACGT 456
Db 1 CTCAGGCGCAGGGAGGAGGACGACGACCAGCAGTCACAGCAGCCCTTGACAAAACGT 60

Qy 457 TCCTGGAATCAAGC 471
Db 61 TCCTGGAATCAAGC 75

RESULT 6
US-10-482-029-240
; Sequence 240, Application US/10482029
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 2974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-240

Query Match      15.9%; Score 75; DB 6; Length 2974;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 397 CTCAGGCGCAGGGAGGAGGACGACGACCAGCAGTCACAGCAGCCCTTGACAAAACGT 456
Db 1 CTCAGGCGCAGGGAGGAGGACGACGACCAGCAGTCACAGCAGCCCTTGACAAAACGT 60

Qy 457 TCCTGGAATCAAGC 471
Db 61 TCCTGGAATCAAGC 75

RESULT 7
US-60-625-561-293
; Sequence 293, Application US/60625561
; GENERAL INFORMATION:
; APPLICANT: MCCAFFREY, Ian
; TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
; FILE REFERENCE: CL001557
; CURRENT APPLICATION NUMBER: US/60/625,561
; CURRENT FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 586
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293
```



```

; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: 10/081,124
; PRIOR FILING DATE: 2002-02-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13996
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3964
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-737-3964

```

Query Match	9.2%	Score 43.2;	DB 6;	Length 366;
Best Local Similarity	86.8%;	Pred. No. 0.018;		
Matches 59;	Conservative 0;	Mismatches 8;	Indels 1;	Gaps 1;
Qy	405	AGAGGGAGGAGACAGCAGACAGACAGTCAACAGCGCCCTTGACAAAC-GTTCTCTGGA	463	
Dd	2	AGAGGTAGGAAGGACAGCAGAGCTGCAGTCAACAGCGCCCTTGACAAGAGAGATTCTCTGGA	61	
Qy	464	ACTCAAGC	471	
Dd	62	GCCCCAAGC	69	

```

RESULT 14
US-10-948-737-3813
; Sequence 3813, Application US/10948737
; GENERAL INFORMATION:
; APPLICANT: CHAN, VIVIEN W.
; APPLICANT: ESCOBEDO JAIME
; APPLICANT: GARCIA, PABLO DOMINGUEZ
; APPLICANT: HANSEN, RHONDA
; APPLICANT: KAUFMANN, JOERG
; APPLICANT: KENNEDY, GIULIA C.
; APPLICANT: LAMSON, GEORGE
; APPLICANT: MOLER, EDWARD J.
; APPLICANT: RANDAZZO, FILIPPO
; APPLICANT: REINHARD, CHRISTOPH
; APPLICANT: SUDDUTH-KLINGER, JULIE
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS III
; FILE REFERENCE: 2300-21987
; CURRENT APPLICATION NUMBER: US/10/948,737
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 10/616,900
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: 09/872,850
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,871
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 10/081,519
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,959
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/310,673
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/336,613
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US03/00657
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/345,637
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: 10/081,124
; PRIOR FILING DATE: 2002-02-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13996
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3813
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-737-3813

```

```

Query Match      9.2%; Score 43.2; DB 6; Length 472;
Best Local Similarity 86.8%; Pred. No. 0.02;
. Matches 59; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 405 AGAGGGAGGAGGACAGCAGACAGTCACAGCAGCCTTGACAAAC-GTTTCTGGGA 463
Db 1 AGAGGTGAGGAGGACAGCAGAGTGTGACAGCAGCCCTGACAGAGAGTTTCTGGGA 60

Qy 464 ACTCAAGC 471
Db 61 GCCCAAGC 68

```

```

RESULT 15
US-10-990-328-95976/c
; Sequence 95976, Application US/10990328
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: US$ THEREOF
; FILE REFERENCE: CL-001495
; CURRENT APPLICATION NUMBER: US/10/990,328
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95976
; LENGTH: 54574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328-95976

```

Query Match	8.3%;	Score 39.4;	DB 6;	Length 54574;
Best Local Similarity	51.6%;	Pred. No. 1.2;		
Matches 114;	Conservative	0;	Mismatches 106;	Indels 1; Gaps 1;
Qy	124	CTCTGTCACAAAGGAAAAATAATCCCCCTGGTGTGACAGACCAGGACAGAACACAGACAG	183	
Db	8846	CTGTGACCCACAGGAGATGGAAACCGTTGTGAAGCCATGTCCTAAAGCA-AAAACAGCTC	8758	
Qy	184	AGGTCAGCATCTGGGGAAGA CAGGTTGTCCTCCAGGGGATGGGGTCCATCCACCTTGGCC	243	
Db	8787	AAGGTGTTTCAGAGGAAAGCTCTCTACCTTCAGAGGGAGGGAGAGGGGAGAAAAAGG	8728	
Qy	244	GAAGAAGATTTCCTGAGGAACTCAAAATACAAGGGAAAAAAGAGGAGGGGACAAAGAGGC	303	
Db	8727	GGATGAGGGGGTGGGGAGGAGAACTGGAGAAAGAGAGGAGGAGAGAAAGAGAGG	8658	
Qy	304	AGAAATGAGAGGGGGAGGACAGAGGACACCTTGAATAAAGA	344	
Db	8667	ACGAGGAAGGGAGAAAGGGAAAGAGGAGAGAAAGATGAAGA	8627	

Search completed: December 11, 2004, 09:55:58
Job time : 160 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 06:27:49 ; Search time 2957 Seconds
(without alignments)
5816.555 Million cell updates/sec

Title: US-10-045-116-1

Perfect score: 472

Sequence: 1 AGCCACACCCAGTGGAGCT.....ACGTTCTCGGAAGTCAAGCA 472

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hrc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	87.8	18.6	328	AW449279	UI-H-B13-
2	78.4	16.6	701	AG307251	Mus muscu
3	75.2	15.9	522	AZ553789	RPCI-23-1
4	71	15.0	588	AZ377232	IM0131P23
5	69.8	14.8	177	CD709204	EST25731
6	69.8	14.8	338	CD708401	EST24928
7	69.8	14.8	338	CD685182	EST1702 h
8	69.8	14.8	555	CD691155	EST7678 h
9	69.8	14.6	595	AL602851	DKFZ686P
10	68.8	14.6	787	AU140869	AU140869
11	67.6	14.3	552	CD686649	EST3170 h
12	67	14.2	220	BM829043	K-EST0101
13	67	14.2	275	BM836430	K-EST0112
14	67	14.2	279	BM752482	K-EST0029
15	67	14.2	355	BM836104	K-EST0111
16	67	14.2	418	BM751932	K-EST0028
17	67	14.2	483	BM828560	K-EST0101
18	67	14.2	569	BM836866	K-EST0112
19	65.4	13.9	310	BX950909	DKFZP781B
20	64.6	13.7	534	BM752131	K-EST0028
21	63	13.3	879	AQ746357	HS-2278_A
22	62.8	13.3	632	CE403021	tigr-gss-
23	62	13.1	195	AW839587	RC6-IT007
24	62	13.1	490	CD618569	56076560V

25	61	12.9	651	1	AL602396	AL602396	DKFZ686P
26	60	12.7	716	6	CD618550	56043842H	
27	60	12.7	729	6	CD618558	56044026H	
28	60	12.7	803	6	CD618546	56043758H	
29	60	12.7	841	6	CD618552	56043850H	
30	59	12.5	390	1	AA132598	z017C08.r	
31	59	12.5	489	6	CD618563	56076536J	
32	59	12.5	579	6	CD618516	56019457H	
33	59	12.5	670	6	CD618510	56019433H	
34	58.4	12.4	548	6	CD618545	56043734J	
35	58.4	12.4	726	6	CD618556	56043910H	
36	58.4	12.4	823	6	CD618555	56043858J	
37	57.6	12.2	512	6	CD696697	EST13220	
38	57.4	12.2	486	6	CD618565	56076544J	
39	57.4	12.2	574	5	BX479959	DKFZ686M	
40	57.2	12.1	557	6	CD691034	EST7557 h	
41	57	12.1	180	6	CD618536	56027690H	
42	56	11.9	887	4	BI759915	603044336	
43	55	11.7	380	1	AA132182	z028B09.r	
44	54.2	11.5	534	6	CD691079	EST7602 h	
45	53.4	11.3	677	6	CD618515	56019449J	

ALIGNMENTS

RESULT 1
AW449279
LOCUS
DEFINITION
UI-H-B13-akh-e-09-0-UI-sl NCI CGAP_Sub5 Homo sapiens cDNA clone
IMAGE:2734193 3', mRNA sequence.
ACCESSION
AW449279
VERSION
AW449279.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 328)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

Location/Qualifiers
1..328
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2734193"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Subs5"
/note="Vector: pTYT3D-Pac (Pharmacia) with a modified
polylinker; Site1: Not 1; Site 2: Eco RI; NCI CGAP_Sub5
is a subtracted library derived from NCI CGAP_Sub4. The
NCI CGAP_Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NCI CGAP_Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)
132276-132391, 1456008-1456775, 1500552-1502855);
NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clones) 1323912-1325831, 1471368-1472903,

1492104-1493255); NCI_CGAP_Lu5 pool 1 L1AM 3575-3582,
 3851-3854 (IMAGE Clones)
 1414920-1417991,1520904-1522439); NCI_CGAP_GC4 pool 1 L1AM
 3164-3167, 3716-3720, 3733-3735 (IMAGE Clones)
 1257096-1258631,1469064-1470983, 1475592-1476743);
 NCI_CGAP_Px22 pool 1 L1AM 2457-2459, 2758-2759, 3062-3068
 (IMAGE Clones) 985608-986759,1101192-1101959,
 1217928-1220615); NCI_CGAP_Co10 pool 1 L1AM 2644-2653,
 2871-2872 (IMAGE Clones)
 1057416-1061255,1144584-1145351). (10% of the driver
 population), plus a pool of 3,840 arrayed clones from
 NCI_CGAP_Sub1 (IMAGE Clones) 2708616-2710535) and
 NCI_CGAP_Sub2 (IMAGE Clones) 2710536-2712455) (10% of
 the driver population), plus a pool of 11,136 clones from
 NCI_CGAP_Sub3 (IMAGE Clones) 2712456-2723591) (10% of the
 driver population), plus a pool of 5,472 clones from
 NCI_CGAP_Sub4 (IMAGE Clones) 2723592-2728969) (70% of the
 driver population). Subtraction was performed as
 previously described [Bonaldo, Lennon & Soares (1996)]:
 Normalization and Subtraction: Two Approaches To
 Facilitate Gene Discovery. Genome Research 6, 791-806.
 TAG_TISSUE=colon
 TAG_LIB=NCI_CGAP_Co10
 TAG_SEQ=AAACG"

ORIGIN

Query Match 18.6%; Score 87.8; DB 2; Length 328;
 Best Local Similarity 65.5%; Pred. No. 6.5e-13;
 Matches 154; Conservative 0; Mismatches 62; Indels 19; Gaps 1;
 QY 1 AGCCACCCAGTCAGCTTTTTCAGCCCCAGAGCCACTCTGTACACCTTCTCTGTG 60
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 35 AGTCATCCCCAGTCAGCTTTTCCATCCCCAGAGCCACTCTGTACACCTTCTCTGTG 94
 QY 61 GGCATCATCCCACTTCCAGAGCCCTGGAGAGCTGGGGAGACCCGGAGCCCTCTGGG 120
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 95 GGTGCTTCTCTACCTTCCAGCACACTGAAGAGCATGGGAGACCTGGCAGCTCACTGT 154
 QY 121 TTTCTCTGTCAAAAGGAAAATAATCCCTCTGG-----TGTCAGAC 161
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 155 TTGCAAGAAAATAATTACCACATTTGGATATGCCAGGTTCTCTGTGTGTCTGTACAG 214
 QY 162 ACCCAGGACAGACACAGCAGCTGACCTGGGGAGACAGCTTGTCTCTCC 216
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 215 ACCCATAGCAGACACATAGAGTCACTGTCTGGAGAGGGGGATCCTCTCTCC 269

RESULT 2

AG307251
 LOCUS Mus musculus molossinus DNA, clone:MSMg01-088106.TJ, genomic survey
 DEFINITION sequence.
 ACCESSION AG307251
 VERSION AG307251.1 GI:47880205
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 BAC end Sequences of Library MSMg01
 Unpublished
 TITLE 2 (bases 1 to 701)
 JOURNAL
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 DIRECT SUBMISSION
 TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
 JOURNAL 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Teukuba Institute, Bio Resource Center.
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp
 PRIMERS
 Sequencing : TJ
 LIBRARY
 Vector : pBACE3.6
 R.Site 1 : EORI
 R.Site 2 : EORI.
 FEATURES
 Location/Qualifiers
 1..701
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 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-088106.TJ"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 16.6%; Score 78.4; DB 9; Length 701;
 Best Local Similarity 56.4%; Pred. No. 2.9e-10;
 Matches 239; Conservative 0; Mismatches 181; Indels 24; Gaps 4;
 QY 23 TTTCAGCCCCAGAGCCACTCTGTACCTTCTCTGTGGGATCATCCACCTTCCAGAG 82
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 173 TTCCAAACTTCACTGGCACCTGTGTCACTTCTTGTCTGGGAA--ATCCACCTTCCAGAG 230
 QY 83 GCCCTGAGAGCATGGGGAGACCCGGAGACCTGTCTGTGGTTCCTGTCTCAGAAAGGAAAT 142
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 231 GTACTGAAGACACAGGGCAGACTAGGAGCTCATCTGGGTCTATGTGTCTCAGGGGCACAT 290
 QY 143 AATCCCCCTGTGT-----TGACAGACCCAGGAGCAGACACAGCAGAGG 186
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 291 AGGAAAGATAGAGTTTCCCTCTTTGATGCTGACAGACTCATGTCCAGGAGTCAGCAGATA 350
 QY 187 TCAGCAGCTGGGAGAGACAGGTTGTCTCCAGGGGATGGGGTCCATCCACCTTGGCGAA 246
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 351 TCAGGCTGGATGAATCATTTTCTCTGAGGGCATGTCGATACTTATCAGCTGTGTTC 410
 QY 247 AAGATTTGTCTGAGAACTGAAATAGAGGAAAGAGAGGAGGAGGAGGAGGAGGAGGAG 306
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 411 TCAAGGTTTGTGGAGAGAAACATAAAGAGAGAAAATTTGAGGAGAGATCGGGGGCAGC 470
 QY 307 AATGAGAGGGGAGGAGCAGAGGA-----CACCTGAATAAAGACACACCCATGACCCAC 361
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 471 ACTGAGAGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 530
 QY 362 GTGATGCTGAGAAATGATCTCTGCTCCCTAGGAGAGACTCAGGGCAGAGGAGGAGGAGGAG 421
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 531 AGGATTTCTGGAGAGTGTCTCTG-CTTGAGAGAAAACCTCAGCTCAGAAAGGAGGAGGAG 589
 QY 422 CAGA 425
 Db | | | |
 590 CAGA 593
 RESULT 3
 AZ553789
 LOCUS RPCI-23-177H11.TJ RPCI-23 Mus musculus genomic clone
 DEFINITION RPCI-23-177H11, genomic survey sequence.
 ACCESSION AZ553789
 VERSION AZ553789.1 GI:11233609
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 522)

AUTHORS
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akınret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C. M.

TITLE
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)

JOURNAL
Other GSRS: RPCI-23-177H11.TV

COMMENT

TITLE
JOURNAL
COMMENT

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (inforesgen.com). BAC end page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html

Plate: 177 row: H column: 11

Seq primer: SP6

Class: BAC ends

FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPC1-23-177H11"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPC1-23"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

```

RIGIN

Query Match	15.9%;	Score 75.2;	DB 8;	Length 522;
Best Local Similarity	55.9%;	Pred. NO. 2e-09;		
Matches 237:	Conservative	0;	Mismatches 163;	Indels 24;
				Gaps 4

23 TTCTAGCCCCAGAGCCACTCTGTCACTTCTCTGTGTGGGCATCATCCCACTTCCCGA 82
24 TTTCTAGCCCCAGAGCCACTCTGTCACTTCTCTGTGTGGGCATCATCCCACTTCCCGA 83
92 TTCCAAACTTCACTGGCACCTGTGTCACTTCTCTGTGTGGGAA--ATCCACACCTTCCCGA 149
93 TTCCAAACTTCACTGGCACCTGTGTCACTTCTCTGTGTGGGAA--ATCCACACCTTCCCGA 150
83 GCCCTGGAGAGCATGGGGACCCGGGACCTCTGGGTTTCTCTGTCAACAAGGAAAT 142
150 GTACTTGAAGACACAGGGCTGTTTGTGATCTCATCTGGGTCATGTGTCTCAGGGACACAT 209
151 GTACTTGAAGACACAGGGCTGTTTGTGATCTCATCTGGGTCATGTGTCTCAGGGACACAT 210
143 AATCCCCCTGGTG-----TGACAGACCCAGGACAGACAGAACACAGACAGG 186
144 AATCCCCCTGGTG-----TGACAGACCCAGGACAGACAGAACACAGACAGG 187
210 AGGAAAGATAGAGGTTCCCTCTTGTGCTGACAGACTCATGTCAGGAGTCTAGCAGATA 269
187 TCAGCACTGGGGAAGACAGGTTGTCTCTCCAGGGATGGGGGTCCATCCACTTGTCCGAA 246
188 TCAGCACTGGGGAAGACAGGTTGTCTCTCCAGGGATGGGGGTCCATCCACTTGTCCGAA 247
270 TCAGCGCCTGGATGAATCATTTGTTCTGAGGGCATGCGATACTTATCATCTGTGTTCG 329
271 TCAGCGCCTGGATGAATCATTTGTTCTGAGGGCATGCGATACTTATCATCTGTGTTCG 330
247 AGATTTTGTCTAGGNACTGGAATAAGAGGGAAGAGAGAGGGGACAAAAGAGGCAGA 306
248 AGATTTTGTCTAGGNACTGGAATAAGAGGGAAGAGAGAGGGGACAAAAGAGGCAGA 307
330 TCAAGGTTTGTGAGAGAAACATAAAGAGAGAAATGTGAGGAAGATTTGGGGCAGC 389
331 TCAAGGTTTGTGAGAGAAACATAAAGAGAGAAATGTGAGGAAGATTTGGGGCAGC 390
307 AATGAGAGGGGAGGGGACAGAGGA-----CACTGTAATAAGACACACCCCATGCCAC 361
308 AATGAGAGGGGAGGGGACAGAGGA-----CACTGTAATAAGACACACCCCATGCCAC 362
390 ACTGAGAGTGGAAAGTGACTGACAGATGTCTGTGGTACAGACCCCAACACACAGCCCAT 449
391 ACTGAGAGTGGAAAGTGACTGACAGATGTCTGTGGTACAGACCCCAACACACAGCCCAT 450
362 GTGATGCTGAGAAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGGAAGGACAG 421
363 GTGATGCTGAGAAGTACTCTCCCTAGGAAGAGACTCAGGGCAGAGGGGAAGGACAG 422
450 AGGATTTCTGGGAAGTGTCTCTG-CCTTGAGAGAAAACCTCAGCTCAGAAGAGAGGAAGCAG 508
451 AGGATTTCTGGGAAGTGTCTCTG-CCTTGAGAGAAAACCTCAGCTCAGAAGAGAGGAAGCAG 509

Qy	422	CAGA	425	
Db	509	CAGA	512	
RESULT 4	AZ377232			
LOCUS	1M0131P23F	Mouse 10kb plasmid	U9C1M library	Mus musculus genomic
DEFINITION				linear GSS 02-OCT-2000
ACCESSION	AZ377232			
VERSION	AZ377232			
KEYWORDS				
SOURCE	AZ377232.1	GI:10490932		
ORGANISM	Mus musculus	(house mouse)		
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
SOURCE				

FEATURES

1. :386
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0131P23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 15.0%; Score 71; DB 8; Length 588;
Best Local Similarity 55.2%; Pred. No. 2.9e-08;
Matches 234; Conservative 0; Mismatches 166; Indels 24; Gaps 4;

QY 23 TTCTAGCCCCCAGAGCCACTCTGTACACCTTCTCTGTGGGCATCATCCACCTTCCCGA 82
|||
Db 98 TTCCAACTGTCAGACATCTGTGCTCCCTTCTCTGATAGGA--AGCTCACCTTCCCGA 155
|||
QY 83 GCCCTGGAGAGCATGGGAGACCCGGGACCTGCTGGGTTCTCTGTCAAAAGGAAAT 142
|||
Db 156 GCTCTGAGGACAAAGTCAGACTGGGACCTCAGCTGGGCTCTGTGTCAAGGGACAGT 215
|||
QY 143 AATCCCTCTGGTG-----TGACAGACCCCAAGGACAGAACACAGAGAGG 186
|||
Db 216 AGGAATGATGGAGGCTCCCTCTTGTGATGCTGACAGACTCATATCTGGGAGTCAGCATATG 275
|||
QY 187 TCAGCACTGGGAGACAGTGTCTCTCCAGGGATGGGGTCCATCCACCTTCCCGA 246
|||
Db 276 TCAGCCCTTGGATGATGTTGTTCTGTGAGGCATGCCGATCTTATCAGCCTTGTTC 335
|||
QY 247 AAGATTTGTTGAGGAACCTGAANAATAGAGGGAAGGAGGAGGACAAAGAGGCGAGA 306
|||
Db 336 TCAAGTCTTGTGGAGGAGATCATAAAGAGAGAAATGTGAGAAAGATGTGTGTCAGC 395
|||
QY 307 AATGAGGGGGAGGAGACAGAGACACCTGAATAAGA-----CCACACCCATGACCCAC 361
|||
Db 396 ACTGAGTGGAGTGAAGTACTTAGCAGTTCTATGGACACAGACCCACCAACACAGCCCAT 455
|||
QY 362 GTGATGCTGAGAGTACTCTCTCCCTAGGAAGAGACTCAGGCAGAGGGAGGAGAGACAG 421
|||
Db 456 AGATTTCTGGAGTGTCTCTG-CCTGAGAGAACACTCAGGTCAAAAGGAGGAGAGACAG 514
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QY 422 CAGA 425
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Db 515 TAGA 518
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RESULT 5
CD709204
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD709204
EST25731 human nasopharynx Homo sapiens linear EST 25-JUN-2003
CD709204
CD709204.1 GI:32239834
EST.
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
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Sun Yat-sen University
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Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

FEATURES
source
1..594
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
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/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cdna
library from southern Chinese"

ORIGIN
Query Match 15.0%; Score 71; DB 6; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 401 GGGCAGAGGGAGGAGGAGCAGCAGACAGTCTGACAGCCTTGACAAAACCTTCTCT 460
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Db 21 GGGCAGAGGGAGGAGGAGCAGCAGACAGTCTGACAGCCTTGACAAAACCTTCTCT 80
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QY 461 GGAACCTCAAGC 471
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Db 81 GGAACCTCAAGC 91
|||
RESULT 6
CD708401
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD708401
EST24928 human nasopharynx Homo sapiens linear EST 25-JUN-2003
CD708401
CD708401.1 GI:32239031
EST.
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
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651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

FEATURES
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cdna
library from southern Chinese"

ORIGIN
Query Match 14.8%; Score 69.8; DB 6; Length 177;
Best Local Similarity 97.3%; Pred. No. 4.5e-08;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 399 CAGGCGAGGGAGGAGGAGCAGCAGACAGTCTGACAGCCTTGACAAAACGTTTC 458
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Db 3 CCGGGAGAGGGAGGAGGAGCAGCAGACAGTCTGACAGCCTTGACAAAACGTTTC 62
|||
QY 459 CTGGAACCTCAAGC 471
|||
Db 63 CTGGAACCTCAAGC 75
|||

RESULT 7
CD685182
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD685182
EST1702 human nasopharynx Homo sapiens linear EST 25-JUN-2003
CD685182
CD685182.1 GI:32200899
EST.
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University

Qy 459 CTGGAACTCAAGC 471
Db 77 CTGGAACTCAAGC 89

Db	1	AGAGGGAGGAGGACGACGACGACGACGCTTCACAGCGCTTGACAAACGTTCTCTGGAA	60
QY	465	CTCAAGC	471
Db	61	CTCAAGC	67

Search completed: December 11, 2004, 08:48:04
Job time : 2960 secs

RESULT 15
BM836104
LOCUS
DEFINITION
K-EST0111597 S9SNU601 Homo sapiens cDNA clone S9SNU601-65-F08 5',
mRNA sequence.
ACCESSION
BM836104
VERSION
BM836104.1 GI:19192513
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
REFERENCE
1 (bases 1 to 355)
AUTHORS
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE
21C Frontier Korean EST Project 2001

JOURNAL
Unpublished (2002)

COMMENT

Contact: Kim YS

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52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

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Email: yongsung@mail.kribb.re.kr

Plate: 65 row: F column: 08

High quality sequence stop: 355.

Location/Qualifiers

1..355

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S9SNU601-65-F08"

/sex="M"

/tissue_type="Ascites"

/cell_type="Epithelial"

/cell_line="SNU-601"

/lab_host="Top10F"

/clone_lib="S9SNU601"

/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;

Site 2: XhoI; The poly (A) + RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including SfiI

site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized with Superscript II using SfiI

oligo-dT primer. After first strand synthesis, RNA was

degraded by NaOH treatment and cDNA was amplified by PCR

reaction. The PCR products were digested with SfiI and

cloned into draIII- digested pME18-FL3 vector. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F, by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

ORIGIN

Query Match 14.2%; Score 67; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	405	AGAGGGAGGAGGACGACGACGACGCTTCACAGCGCTTGACAAACGTTCTCTGGAA	464
Db	1	AGAGGGAGGAGGACGACGACGCTTCACAGCGCTTGACAAACGTTCTCTGGAA	60

QY	465	CTCAAGC	471
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